



STiC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100503

TO: Konstantina Katcheves
Location: CM1/11C01/11E12 /
Art Unit: 1636
Friday, August 08, 2003

Case Serial Number: 09/846797

From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

See attached results.

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith
308-3278

180 523

STIC-Biotech/ChemLib

RECEIVED

AUG-5 2003

(STIC)

From: Fredman, Jeffrey
Sent: Tuesday, August 05, 2003 11:24 AM
To: STIC-Biotech/ChemLib
Cc: Katcheves, Konstantina
Subject: FW: RUSH sequence search 09/846797
 PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Katcheves, Konstantina
Sent: Monday, August 04, 2003 3:26 PM
To: Fredman, Jeffrey
Subject: RUSH sequence search 09/846797

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
 Tina

Konstantina Katcheves
Art Unit 1636
Phone: 305-1999
Office: 11B15
Mailbox: 11E12

M, SM, TN

21A

8/5/03

8/8/03

3
5
5

8/5/03

Katcheves, Konstantina

Fr m: Fredman, Jeffrey
S nt: Tuesday, August 05, 2003 11:24 AM
To: STIC-Biotech/ChemLib
Cc: Katcheves, Konstantina
Subject: FW: RUSH sequence search 09/846797

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Katcheves, Konstantina
Sent: Monday, August 04, 2003 3:26 PM
T : Fredman, Jeffrey
Subject: RUSH sequence search 09/846797

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
Tina

Konstantina Katcheves
Art Unit 1636
Phone: 305-1999
Office: 11B15
Mailbox: 11E12

8/5/03

Katcheves, Konstantina

To: Fredman, Jeffrey

Subject: RUSH sequence search 09/846797

2/1/03

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
Tina

Konstantina Katcheves

Art Unit 1636

Phone: 305-1999

Office: 11B15

Mailbox: 11E12

8/4/03

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 22:51:21 Search time 1893.28 Seconds
(without alignments)
449.303 Million cell updates/sec

Title: US-09-846-797-6
Perfect score: 35
Sequence: 1 ctatgcgcataagttatggttaagactacacg 35

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	157	12	BM870744	
2	100.0	163	9	AU007416	BM870744 mgns01xm
3	100.0	177	9	AU010787	AU007416 AU007416
4	100.0	184	9	AU010656	AU010787 AU010787
					AU010656 AU010656

5	100.0	184	9	AU010788	AU010788 AU010788
6	100.0	184	9	AU010834	AU010834 AU010834
7	100.0	184	9	AU010835	AU010835 AU010835
8	100.0	195	9	AU011658	AU011658 AU011658
9	100.0	195	9	AU011659	AU011659 AU011659
10	100.0	196	9	AU007372	AU007372 AU007372
11	100.0	197	9	AU009140	AU009140 AU009140
12	100.0	224	28	A2931573	A2931573 474.dh286
13	100.0	237	9	AU007492	AU007492 AU007492
14	100.0	236	9	A1904526	A1904526 PM-BT057-
15	100.0	316	9	A1904469	A1904469 PM-BT057-
16	100.0	317	9	A1904470	A1904470 PM-BT057-
17	100.0	339	9	AU792106	AU792106 D01007-R
18	100.0	349	12	BM958701	BM958701 PLATE-10
19	100.0	356	13	B0751733	B0751733 EST632296
20	100.0	360	9	AJ500769	AJ500769 AJ500769
21	100.0	365	12	BM131461	BM131461 T9ESTY69
22	100.0	381	28	A2931738	A2931738 474.dh289
23	100.0	384	14	CD456349	CD456349 F903_03g1
24	100.0	418	12	BM004286	BM004286 T9ESTY68
25	100.0	425	9	AJ499444	AJ499444 AJ499444
26	100.0	430	9	AW791124	AW791124 D00413-R
27	100.0	430	14	CD035900	CD035900 mgmto11xj
28	100.0	431	13	BQ143267	BQ143267 fmh1c.pk0
29	100.0	433	9	AW792634	AW792634 D01303-F
30	100.0	438	28	A2929878	A2929878 479.dh156
31	100.0	440	28	A2930332	A2930332 474.dh253
32	100.0	443	13	B0784402	B0784402 SNEST4875
33	100.0	456	13	B0751734	B0751734 EST632297
34	100.0	466	28	BH677706	BH677706 BOME04TF
35	100.0	457	13	BQ498557	BQ498557 EST07782
36	100.0	457	13	B0750940	B0750940 EST631503
37	100.0	457	28	A2929872	A2929872 479.dh156
38	100.0	473	29	CNS06X7D	AL420167 77 end of
39	100.0	478	28	A2930146	A2930146 474.dh250
40	100.0	493	14	CD037449	CD037449 mgscu011x8
41	100.0	495	12	BM131374	BM131374 T9ESTY69
42	100.0	496	28	A2930737	A2930737 474.dh258
43	100.0	497	10	BF251968	BF251968 EST419230
44	100.0	500	28	A2931163	A2931163 474.dh262
45	100.0	502	14	CB383239	CB383239 T9ESTY68

ALIGNMENTS

RESULT 1
BM870744/c
LOCUS
DEFINITION
mgns01xm14f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe
grisea cDNA clone mgns01xm14 5', mRNA sequence.

ACCESSION
BM870744
VERSION
BM870744.2 GI:30404361
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea

REFERENCE
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.

AUTHORS
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai
K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea

TITLE
Unpublished
COMMENT
On Mar 7, 2002 this sequence version replaced gi:19338426.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person

Best nr hit (April. 22, 2003) refine_701347.11 hypothetical
 protein [plasmodium falciparum 3D7]... 44 5e-04
 PCR primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgn5011 row: M column: 14
 Seq primer: T3.
 Location/Qualifiers

FEATURES

source

1. 157
 /organism="Magnetoprote grisea"
 /mol_type="mRNA"
 /strain="Guy11"
 /db_xref="taxon:148305"
 /clone="mgn5011xm14"
 /sex="Mati-2 hermaphrodite"
 /cell_type="mycelium"
 /clone_lib="Magnetoprote grisea NS Uni-Zap XR Library"
 /note="Vector: BluescriptSK-; Site_1: EcoRI; Site_2: XhoI
 ; Unidirectional cloning. EcoRI site has T3 primer and
 predominantly 5' reads. T7 primer on XhoI side of insert.
 Nitrogen starvation library. Cells were inoculated into
 minimal medium and grown for two days with shaking (150
 rpm) at room temperature. Culture was harvested, blended,
 inoculated into minimal medium as above for 24 h. Cells
 were harvested, washed with water and inoculated into
 minimal medium base lacking nitrogen source for 6 h.
 Sequences were processed by one of two methods. Where a
 full-length alignment to the M. grisea genome sequence was
 available, the EST sequence was trimmed according to the
 alignment, otherwise sequence quality was assessed using
 phredphrap version 991019 and trimmed according to phd
 files (0.05) and for vector seqs."

BASE COUNT

44 a 31 c 39 g 43 t

ORIGIN

Query Match 100.0%; Score 35; DB 12; Length 157;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 Db 93 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 59

RESULT 2

A0007416

LOCUS A0007416 163 bp mRNA linear EST 31-JUL-1998
 DEFINITION A0007416 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc01943, mRNA sequence.

ACCESSION

A0007416

VERSION A0007416.1 GI:3343874
 EST
 Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 1 (bases 1 to 163)
 Morimyo,M. and Mita,K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe

SOURCE

ORGANISM

REFERENCE
 AUTHORS Morimyo,M. and Mita,K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces
 pombe

JOURNAL

COMMENT

Unpublished
 Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers

FEATURES

source

1. 163
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"

/clone="spc01943"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT

46 a 37 c 33 g 47 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 163;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 Db 68 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 102

RESULT 3

A010787

LOCUS A010787 177 bp mRNA linear EST 31-JUL-1998
 DEFINITION A010787 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc10371, mRNA sequence.

ACCESSION

A010787

VERSION A010787.1 GI:3347467
 EST
 Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 1 (bases 1 to 177)
 Morimyo,M. and Mita,K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe

SOURCE

ORGANISM

REFERENCE
 AUTHORS Morimyo,M. and Mita,K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces
 pombe

JOURNAL

COMMENT

Unpublished
 Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers

FEATURES

source

1. 177
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10371"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT

46 a 38 c 34 g 55 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 177;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 Db 61 CTAGTCGGCATGTTATGTTAGTAACTACGACGG 95

RESULT 4
 A010656

LOCUS AU010656 184 bp mRNA linear EST 31-JUL-1998
 DEFINITION AU010656 Schizosaccharomyces pombe late log phase cDNA
 ACCESSION AU010656
 VERSION AU010656
 KEYWORDS EST
 SOURCE AU010656.1 GI:3347336
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Moriyoshi, M. and Mita, K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished
 COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1.184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10200"
 /sex="h minus"
 /clone_id="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 ||||||||||||||||||||||||||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

RESULT 5 184 bp mRNA linear EST 31-JUL-1998
 AU010788
 LOCUS AU010788
 DEFINITION AU010788 Schizosaccharomyces pombe late log phase cDNA
 ACCESSION AU010788
 VERSION AU010788
 KEYWORDS EST
 SOURCE AU010788.1 GI:3347468
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Morimyo, M. and Mita, K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished
 COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1.184

FEATURES

source

/organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10372"
 /sex="h minus"
 /clone_id="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 ||||||||||||||||||||||||||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

RESULT 6 184 bp mRNA linear EST 31-JUL-1998
 AU010834
 LOCUS AU010834
 DEFINITION AU010834 Schizosaccharomyces pombe late log phase cDNA
 ACCESSION AU010834
 VERSION AU010834
 KEYWORDS EST
 SOURCE AU010834.1 GI:3347514
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Morimyo, M. and Mita, K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished
 COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1.184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10423"
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 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 ||||||||||||||||||||||||||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

RESULT 7
LOCUS AU010835 184 bp mRNA linear EST 31-JUL-1998
DEFINITION AU010835 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU010835 Schizosaccharomyces pombe cDNA clone spc10424, mRNA sequence.
VERSION AU010835
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 184)
TITLE Morimyo, M. and Mita, K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
 1..184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10424"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 48 a 42 c 38 g 56 t
ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTTATGTTAGACTACGACG 35
 ||||||||||||||||||||||||||||||||
Db 68 CTAGTCGCATAGTTTATGTTAGACTACGACG 102

RESULT 8
LOCUS AU011658 195 bp mRNA linear EST 03-AUG-1998
DEFINITION AU011658 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU011658 Schizosaccharomyces pombe cDNA clone spc11806, mRNA sequence.
VERSION AU011658
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 195)
TITLE Morimyo, M. and Mita, K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences

FEATURES 9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan
SOURCE Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1..195
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11806"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 63 a 36 c 43 g 52 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTTATGTTAGACTACGACG 35
 ||||||||||||||||||||||||||||||||
Db 138 CTAGTCGCATAGTTTATGTTAGACTACGACG 104

RESULT 9
LOCUS AU011659 195 bp mRNA linear EST 03-AUG-1998
DEFINITION AU011659 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU011659 Schizosaccharomyces pombe cDNA clone spc11807, mRNA sequence.
VERSION AU011659
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 195)
TITLE Morimyo, M. and Mita, K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
 1..195
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11807"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 63 a 36 c 43 g 52 t 1 others
ORIGIN

QY 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
 |||||||
 Db 138 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 104

RESULT 10
 AU007372 196 bp mRNA linear EST 31-JUL-1998
 LOCUS AU007372 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION Schizosaccharomyces pombe cDNA clone spc01850, mRNA sequence.
 ACCESSION AU007372
 VERSION AU007372.1 GI:3343830
 SOURCE EST.
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 1 (bases 1 to 196)
 Morimyo, M. and Mita, K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe
 JOURNAL Unpublished
 COMMENT Contact: Mitsunoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1. 196
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc01850"
 /sex="h minus"
 /note="Vector: M13mp19. The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 59 a 37 c 45 g 55 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 196;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
 |||||||
 Db 129 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 95

RESULT 11
 AU009140 197 bp mRNA linear EST 31-JUL-1998
 LOCUS AU009140 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION Schizosaccharomyces pombe cDNA clone spc04530, mRNA sequence.
 ACCESSION AU009140
 VERSION AU009140.1 GI:3345820
 SOURCE EST.
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 1 (bases 1 to 197)
 Morimyo, M. and Mita, K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe

JOURNAL Unpublished
 COMMENT Contact: Mitsunoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1. 197
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc04530"
 /sex="h minus"
 /note="Vector: M13mp19. The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 55 a 45 c 38 g 59 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 197;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
 |||||||
 Db 68 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 102

RESULT 12
 A2931573 224 bp DNA linear GSS 01-APR-2001
 LOCUS A2931573 474.dhz86c05.s1 Saccharomyces unisporus NRRL Y-1556 Saccharomyces
 DEFINITION unisporus genomic clone 474.dhz86c05.s1, genomic survey sequence.
 ACCESSION A2931573
 VERSION A2931573.1 GI:13502484
 SOURCE GSS.
 ORGANISM Saccharomyces unisporus
 Saccharomyces unisporus
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 1 (bases 1 to 224)
 Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Glsh
 M.R., Waterston, R.H. and Johnston, M.
 Surveying Saccharomyces genomes to identify functional elements by
 comparative DNA sequence analysis
 JOURNAL Unpublished
 COMMENT Contact: Johnston M
 Department of Genetics
 Washington University Medical School
 Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
 Tel: 314 362 2735
 Fax: 314 362 7835
 Email: mjgenetics.wustl.edu
 Class: random plasmid subclone.
 Location/Qualifiers
 1. 224
 /organism="Saccharomyces unisporus"
 /mol_type="genomic DNA"
 /strain="NRRL Y-1556 (CBS 398)"
 /db_xref="taxon:27294"
 /clone="474.dhz86c05.s1"
 /clone_lib="Saccharomyces unisporus NRRL Y-1556"
 /note="Random genomic sequence"

BASE COUNT 67 a 40 c 60 g 57 t

ORIGIN

Query Match 100.0%; Score 35; DB 28; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 35: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGGCATAGTTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 111 CTAGTCGGCATAGTTTATGTTAGACTACGACG 77

RESULT 13
 A0007492 237 bp mRNA linear EST 31-JUL-1998
 LOCUS A0007492 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION A0007492 Schizosaccharomyces pombe cDNA clone spc02102, mRNA sequence.
 ACCESSION A0007492
 VERSION A0007492.1 GI:3343950
 KEYWORDS EST.
 SOURCE Schizosaccharomyces pombe (filson yeast)
 ORGANISM Schizosaccharomyces pombe (filson yeast)
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 1 (bases 1 to 237)
 Morimyo M. and Mita K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe
 JOURNAL Unpublished
 COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Arima-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1..237
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc02102"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19. The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 65 a 58 c 44 g 67 t 3 others

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 237;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGGCATAGTTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 68 CTAGTCGGCATAGTTTATGTTAGACTACGACG 102

RESULT 14
 A1904526 296 bp mRNA linear EST 30-MAR-2000
 LOCUS A1904526 PM-BT057-290199-289 BT057 Homo sapiens cDNA, mRNA sequence.
 DEFINITION A1904526
 ACCESSION A1904526
 VERSION A1904526.1 GI:6494913
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 296)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 MEDLINE 10737800
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?cl=PM-BT057-289.html>
 &ls=290199<=1)
 Seq primer: puc 18 forward.
 Location/Qualifiers
 1..296
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
 /clone_lib="BT057"
 /note="Organ: breast; Vector: puc18; Site:1; SmaI; Site:2;
 SmaI: A mini-library was made by cloning products derived
 from ORESTES PCR (O.S. Letters Patent Application No. 196
 '716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 88 a 56 c 78 g 74 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 296;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGGCATAGTTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 128 CTAGTCGGCATAGTTTATGTTAGACTACGACG 94

RESULT 15
 A1904469 316 bp mRNA linear EST 30-MAR-2000
 LOCUS A1904469 PM-BT057-100299-389 BT057 Homo sapiens cDNA, mRNA sequence.
 DEFINITION A1904469
 ACCESSION A1904469
 VERSION A1904469.1 GI:6494856
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 316)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 MEDLINE 10737800
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/seq/gethtml.pl?tl=PM&t2=PM-BT057-389.html>
ct3-100299&t4=1)

Seq primer: puc18 forward.

Location/Qualifiers

FEATURES

source

1. .316

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/sex="female"

/dev_stage="Adult"

/clone_lib="BT057"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the pUC18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

74 a 87 c 66 g 89 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

35; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

0;

100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

0;

100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

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100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

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100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

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100.0%; Score 35; DB 9; Length 316;

100.0%; Pred. No. 0.00018;

0; Mismatches

0; Indels

0; Gaps

Search completed: August 7, 2003, 00:28:29

Job time : 1896.28 secs

QY 1 CTAGTCGGCATAGTTATGCTTAACACTACGACGG 35
|||||
Db 190 CTAGTCGGCATAGTTATGCTTAACACTACGACGG 224

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:25:31 ; Search time 218.75 Seconds
(without alignments)
431.910 Million cell updates/sec

Title: US-09-846-797-6

Perfect score: 1 ctatcgccatagttatgttaagactacgagc 35

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues 5105512

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	35	24	AAI70914
2	35	100.0	51	21	AAA94981
3	35	100.0	51	21	AAA94985
4	35	100.0	52	21	AAA94978
5	35	100.0	52	21	AAA94979
6	35	100.0	52	21	AAA94980
7	35	100.0	52	21	AAA94983
8	35	100.0	75	24	ABA99904

9	35	100.0	113	24	AAI70915
10	35	100.0	113	24	AAI70916
11	35	100.0	421	22	AAH21226
12	35	100.0	429	22	AAH21229
13	35	100.0	431	22	AAH21230
14	35	100.0	432	22	AAH21228
15	35	100.0	444	22	AAH21227
16	35	100.0	445	22	AAH21231
17	35	100.0	553	25	ABZ54040
18	35	100.0	579	22	AA508601
19	35	100.0	933	15	AAO71716
20	35	100.0	951	18	AAI59946
21	35	100.0	1024	21	AAE11316
22	35	100.0	1228	25	ABZ60030
23	35	100.0	1727	24	ABV78726
24	35	100.0	1731	25	AAI68286
25	35	100.0	1731	24	ABA01154
26	35	100.0	1733	20	AAZ00859
27	35	100.0	1745	24	ABA01152
28	35	100.0	1747	16	AAO94231
29	35	100.0	1747	19	AAV00075
30	35	100.0	1747	21	AAA94191
31	35	100.0	1761	24	ABV78659
32	35	100.0	1766	24	ABV78702
33	35	100.0	1766	24	ABV78705
34	35	100.0	1766	24	ABV78708
35	35	100.0	1766	24	ABV78711
36	35	100.0	1766	24	ABV78714
37	35	100.0	1766	24	ABV78717
38	35	100.0	1766	24	ABV78720
39	35	100.0	1766	24	ABV78723
40	35	100.0	1766	22	AAE25849
41	35	100.0	1798	22	AAO14004
42	35	100.0	1798	22	AAO14297
43	35	100.0	1802	22	AAE23018
44	35	100.0	2055	25	ABZ20766
45	35	100.0	2089	25	ABZ20764

ALIGNMENTS

RESULT 1
AAI70914 standard; DNA; 35 BP.

AAI70914;
12-MAR-2002 (first entry)

Helper oligonucleotide CAI1005 for *Candida* spp. detection.

Candida albicans; *Candida tropicalis*; *Candida dubliniensis*;
Candida viswanathii; *Candida parapsilosis*; detection; ss.

Candida albicans.

WO200183821-A2.
08-NOV-2001.

01-MAY-2001; 2001WO-US13884.
01-MAY-2000; 2000US-201249P.

(GENP-) GEN-PROBE INC.
Hogan JF, Gordon PC;
WPI; 2002-065537/09.

Novel oligonucleotide sequences that are fully complementary to
ribosomal RNA or DNA of *Candida* species; useful for detecting presence

PT of C. albicans, C. dubliniensis, C. viswanathii, C. parapsilosis in test
sample -
PS Claim 2; Page 26; 33pp; English.
XX
CC The present sequence is that of helper oligonucleotide
CC CALA1006, which binds target Candida spp. ribosomal RNA molecules
CC at a site immediately adjacent to probe CALA1038 (see AA170913).
CC The helper oligonucleotide promotes the highly specific
CC hybridisation of CALA1038 probe to a sequence found in the 18S rRNA
CC of Candida albicans, Candida tropicalis, Candida dubliniensis,
CC Candida viswanathii and Candida tropicalis. Probe CALA1038 can
CC distinguish these Candida species from their known phylogenetically
CC nearest neighbours, and is useful for their detection and
CC quantitation. The Tm of interaction between probe and C. albicans
CC rRNA increased from 57.8 to 62.2 degrees C when the helper
CC oligonucleotide was added to the hybridisation reaction, and
CC increased to 63.2 degrees C when another helper oligonucleotide,
CC CALA1066 (see AA170912), was also included.
XX
SQ Sequence 35 BP; 9 A; 6 C; 10 G; 10 T; 0 other;

Query Match 100.0%; Score 35; DB 24; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35

RESULT 2
AAA94981/C
ID AAA94981 standard; DNA; 51 BP.
XX
AC AAA94981;
XX
DT 10-JAN-2001 (first entry)
XX
DE S. arleticantis small ribosomal subunit nucleotide sequence fragment #81.
XX
KW Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
XX EPM; diagnosis; ds.
XX
OS S. arleticantis.
XX
PN US6110665-A.
XX
PD 29-AUG-2000.
XX
PE 14-FEB-1995; 95US-0388029.
XX
PR 14-FEB-1995; 95US-0388029.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
XX WPI; 2000-586347/55.
XX
DR
XX
PT Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
PT presence of S. neuropa in equine blood or cerebrospinal fluid -
PS
XX
PS Disclosure; Fig 1; 41pp; English.
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
CC primer is unique to the S. neuropa species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of S. neuropa is indicative of EPM. To find a
CC sequence unique to S. neuropa small ribosomal subunit sequences from
CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capicantis, S.

CC arleticantis, S. cruzi, S. tenella, E. tenella and C. parvum were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
XX
SQ Sequence 51 BP; 17 A; 12 C; 11 G; 11 T; 0 other;

Query Match 100.0%; Score 35; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 49 CTAGTCGCATAGTTATGTTAGACTACGACG 15

RESULT 3
AAA94985/C
ID AAA94985 standard; DNA; 51 BP.
XX
AC AAA94985;
XX
DT 10-JAN-2001 (first entry)
XX
DE T. gondii small ribosomal subunit nucleotide sequence fragment #85.
XX
KW Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
XX EPM; diagnosis; ds.
XX
OS T. gondii.
XX
PN US6110665-A.
XX
PD 29-AUG-2000.
XX
PE 14-FEB-1995; 95US-0388029.
XX
PR 14-FEB-1995; 95US-0388029.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
XX WPI; 2000-586347/55.
XX
DR
XX
PT Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
PT presence of S. neuropa in equine blood or cerebrospinal fluid -
PS
XX
PS Disclosure; Fig 1; 41pp; English.
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
CC primer is unique to the S. neuropa species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of S. neuropa is indicative of EPM. To find a
CC sequence unique to S. neuropa small ribosomal subunit sequences from
CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capicantis, S.
CC arleticantis, S. cruzi, S. tenella, E. tenella and C. parvum were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
XX
SQ Sequence 51 BP; 17 A; 12 C; 11 G; 11 T; 0 other;

Query Match 100.0%; Score 35; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 49 CTAGTCGCATAGTTATGTTAGACTACGACG 15

RESULT 4

AAA94978/c
 ID AAA94978 standard; DNA; 52 BP.
 XX
 AC AAA94978;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE S. neuropa small ribosomal subunit nucleotide sequence fragment #78.
 XX
 KM Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
 XX EPM; diagnosis; ds.
 OS S. neuropa.
 XX
 PN US6110665-A.
 XX
 PD 29-AUG-2000.
 XX
 PF 14-FEB-1995; 95US-0388029.
 XX
 PR 14-FEB-1995; 95US-0388029.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
 XX WPI; 2000-586347/55.
 XX
 DR Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
 XX testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
 PT presence of S. neuropa in equine blood or cerebrospinal fluid -
 XX
 PS Disclosure; Fig 1; 41pp; English.
 XX
 CC The present invention relates to a diagnostic primer from positions
 CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
 CC primer is unique to the S. neuropa species. The primer is useful for
 CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
 CC the presence of S. neuropa is indicative of EPM. To find a
 CC sequence unique to S. neuropa small ribosomal subunit sequences from
 CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capricanis, S.
 CC arlicanalis, S. cruzi, S. tenella, E. tenella and C. parvum were
 CC compared. The present sequence is a fragment of the small ribosomal
 CC subunit used in this comparison.
 XX
 SO Sequence 52 BP; 18 A; 12 C; 11 G; 11 T; 0 other;
 XX
 QY Query Match 100.0%; Score 35; DB 21; Length 52;
 XX Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
 50 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 16
 XX
 RESULT 5
 ID AAA94979 standard; DNA; 52 BP.
 XX
 AC AAA94979;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE S. muris small ribosomal subunit nucleotide sequence fragment #79.
 XX
 KM Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
 XX EPM; diagnosis; ds.
 OS S. muris.
 XX
 PN US6110665-A.
 XX

PD 29-AUG-2000.
 XX
 PF 14-FEB-1995; 95US-0388029.
 XX
 PR 14-FEB-1995; 95US-0388029.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
 XX WPI; 2000-586347/55.
 XX
 DR Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
 XX testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
 PT presence of S. neuropa in equine blood or cerebrospinal fluid -
 XX
 PS Disclosure; Fig 1; 41pp; English.
 XX
 CC The present invention relates to a diagnostic primer from positions
 CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
 CC primer is unique to the S. neuropa species. The primer is useful for
 CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
 CC the presence of S. neuropa is indicative of EPM. To find a
 CC sequence unique to S. neuropa small ribosomal subunit sequences from
 CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capricanis, S.
 CC arlicanalis, S. cruzi, S. tenella, E. tenella and C. parvum were
 CC compared. The present sequence is a fragment of the small ribosomal
 CC subunit used in this comparison.
 XX
 SO Sequence 52 BP; 18 A; 12 C; 11 G; 11 T; 0 other;
 XX
 QY Query Match 100.0%; Score 35; DB 21; Length 52;
 XX Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
 50 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 16
 XX
 RESULT 6
 ID AAA94980 standard; DNA; 52 BP.
 XX
 AC AAA94980;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE S. capricanis small ribosomal subunit nucleotide sequence fragment #80.
 XX
 KM Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
 XX EPM; diagnosis; ds.
 OS S. capricanis.
 XX
 PN US6110665-A.
 XX
 PD 29-AUG-2000.
 XX
 PF 14-FEB-1995; 95US-0388029.
 XX
 PR 14-FEB-1995; 95US-0388029.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
 XX WPI; 2000-586347/55.
 XX
 DR Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
 XX testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
 PT presence of S. neuropa in equine blood or cerebrospinal fluid -
 XX

PS Disclosure; Fig 1; 41pp; English.
 CC The present invention relates to a diagnostic primer from positions
 CC 1470-1487 of the small ribosomal subunit of Sarcocystis neurona. This
 CC primer is unique to the S. neurona species. The primer is useful for
 CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
 CC the presence of S. neurona is indicative of EPM. To find a
 CC sequence unique to S. neurona small ribosomal subunit sequences from
 CC S. neurona, S. muris, S. gigantea, T. gondii, S. capicantus, S.
 CC arleticantus, S. cruzi, S. tenella, E. tenella and C. parvum were
 CC compared. The present sequence is a fragment of the small ribosomal
 CC subunit used in this comparison.
 SQ Sequence 52 BP; 17 A; 12 C; 11 G; 11 T; 1 other;
 Query Match 100.0%; Score 35; DB 21; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 50 CTACTCGCATAGTTATGTTAAGACTACGACGG 16
 RESULT 7
 ID AAA94983 standard; DNA: 52 BP.
 AC AAA94983;
 DT 10-JAN-2001 (first entry)
 DE S. gigantea small ribosomal subunit nucleotide sequence fragment #83.
 DE Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
 DE EPM; diagnosis; ds.
 KW S. gigantea.
 OS
 XX US6110665-A.
 PN 29-AUG-2000.
 PD 14-FEB-1995; 95US-0388029.
 PF 14-FEB-1995; 95US-0388029.
 PR 14-FEB-1995; 95US-0388029.
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX Fenger CK, Gajedhar AA, Dubey JP, Granstrom DE;
 PI WPI: 2000-586347/55.
 DR Sarcocystis neurona diagnostic primer, useful for in vitro diagnostic
 PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
 PT presence of S. neurona in equine blood or cerebrospinal fluid -
 XX Disclosure; Fig 1; 41pp; English.
 PS
 CC The present invention relates to a diagnostic primer from positions
 CC 1470-1487 of the small ribosomal subunit of Sarcocystis neurona. This
 CC primer is unique to the S. neurona species. The primer is useful for
 CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
 CC the presence of S. neurona is indicative of EPM. To find a
 CC sequence unique to S. neurona small ribosomal subunit sequences from
 CC S. neurona, S. muris, S. gigantea, T. gondii, S. capicantus, S.
 CC arleticantus, S. cruzi, S. tenella, E. tenella and C. parvum were
 CC compared. The present sequence is a fragment of the small ribosomal
 CC subunit used in this comparison.
 SQ Sequence 52 BP; 18 A; 12 C; 11 G; 11 T; 0 other;
 Query Match 100.0%; Score 35; DB 21; Length 52;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 50 CTAGTCGCATAGTTATGTTAAGACTACGACGG 16
 RESULT 8
 ID ABA99904 standard; DNA: 75 BP.
 AC ABA99904;
 DT 17-JUN-2002 (first entry)
 DE C. albicans 18S RNA detecting multiplex probe SEQ ID 6.
 DE 18S RNA; multiplex PCR; probe; detection; amplification;
 DE fungal infection; pathogenic; ss.
 KW Candida albicans.
 OS
 XX WO200227021-A2.
 PN 04-APR-2002.
 PD 24-SEP-2001; 2001WO-EP11023.
 PF 26-SEP-2000; 2000DE-1048009.
 PR (CYTO-) CYTONET GMBH & CO KG.
 PA Boettger EC, Rosenau J, Kirschner P, Jack T;
 PI WPI: 2002-330101/36.
 DR Multiplex amplification for detecting fungal infection, selective for
 PT clinically important strains of Candida and Aspergillus, comprises
 PT amplifying a region of the 18S RNA gene -
 XX Claim 13; Page 27; 27pp; German.
 PS
 CC This invention describes a novel multiplex amplification reaction for
 CC detecting clinically relevant fungal infections by amplifying a region of
 CC the 18S RNA gene, where either sequences from pathogenic Candida and
 CC Aspergillus species are amplified. The method is quick, simple and
 CC sensitive, and can detect all clinically important Candida and
 CC Aspergillus species, but generally it does not detect species commonly
 CC present in laboratories as contaminants (avoiding false positive
 CC results). The detection limit is 3-20 cells/10 ml of blood, depending on
 CC the detection method used. This sequence represents a probe used in
 CC the method of the invention.
 SQ Sequence 75 BP; 15 A; 20 C; 14 G; 25 T; 1 other;
 Query Match 100.0%; Score 35; DB 24; Length 75;
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 ||||||||||||||||||||||||||||||||
 8 CTAGTCGCATAGTTATGTTAAGACTACGACGG 42
 RESULT 9
 ID AAI70915 standard; DNA: 113 BP.
 AC AAI70915;
 DT 12-MAR-2002 (first entry)
 XX

DE Candida species 18S ribosomal DNA probe domain.
XX
KW Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
OS Candida albicans.
XX
PN WO200183821-A2.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US13884.
XX
PR 01-MAY-2000; 2000US-201249P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Hogan JJ, Gordon PC;
XX
DR WPI; 2002-066537/09.
XX
PT Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C. albicans, C. dubliniensis, C. viswanathii, C. parapsilosis in test
PT sample -
XX
PS Claim 1; Page 32; 33pp; English.
XX
CC The present sequence is that of DNA corresponding to a unique
CC segment (see AA170916) of the 18S ribosomal RNA of Candida albicans,
CC Candida tropicalis, Candida dubliniensis, Candida viswanathii and
CC oligonucleotides (see AA170909-14) correspond to a portion of this
CC sequence or its complement. The probes are highly specific, and can
CC distinguish these Candida species from their known phylogenetically
CC nearest neighbours. They are useful for detection and quantitation.
XX
SQ Sequence 113 BP; 35 A; 27 C; 23 G; 28 T; 0 other;
XX
Query Match 100.0%; Score 35; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGTAACTACGACG 35
Db 70 CTAGTCGCATAGTTATGTTAGTAACTACGACG 104
XX
RESULT 10
AA170916/C
ID AA170916 standard; rRNA; 113 BP.
XX
AC AA170916;
XX
DT 13-MAR-2002 (first entry)
XX
DE Candida species 18S ribosomal RNA probe domain.
XX
KW Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
OS Candida albicans.
XX
PN WO200183821-A2.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US13884.
XX
PR 01-MAY-2000; 2000US-201249P.
XX
PA (GENP-) GEN-PROBE INC.
XX

PI Hogan JJ, Gordon PC;
XX
DR WPI; 2002-066537/09.
XX
PT Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C. albicans, C. dubliniensis, C. viswanathii, C. parapsilosis in test
PT sample -
XX
PS Disclosure; Page 32; 33pp; English.
XX
CC The present sequence is that of a unique segment of the 18S
CC ribosomal RNA of Candida albicans, Candida tropicalis,
CC Candida dubliniensis, Candida viswanathii and Candida tropicalis.
CC Claimed hybridisation probes and helper oligonucleotides (see
CC AA170909-14) correspond to a portion of this sequence or its
CC complement. The probes are highly specific, and can distinguish
CC these Candida species from their known phylogenetically nearest
CC neighbours. They are useful for detection and quantitation.
XX
SQ Sequence 113 BP; 28 A; 23 C; 27 G; 35 U; 0 other;
XX
Query Match 100.0%; Score 35; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGTAACTACGACG 35
Db 44 CTAGTCGCATAGTTATGTTAGTAACTACGACG 10
XX
RESULT 11
AAH21226/C
ID AAH21226 standard; DNA; 421 BP.
XX
AC AAH21226;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. krusei 16S rRNA DNA fragment YSARSUD.
XX
KW Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KW food monitoring; water monitoring; veterinary; forensic; primer; probe;
KW detection; ss.
XX
OS Candida krusei.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-DE04610.
XX
PR 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEF A.
PA (STUE/) STUEBER F.
PI Hoeft A, Stueber F;
XX
DR WPI; 2001-425677/45.
XX
PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides -
XX
PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (I) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (I) from the physical properties of the (I)-ON complex, e.g.

CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the
CC invention.

XX
SQ Sequence 421 BP; 109 A; 88 C; 115 G; 104 T; 5 other;

Query Match 100.0%; Score 35; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
DB 376 CTAGTCGCATAGTTATGTTAAGACTACGACGG 342
|||||

RESULT 12
AAH21229/c
ID AAH21229 standard; DNA: 429 BP.
XX
AC AAH21229;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. tropicalis 16S rRNA DNA fragment YSASRSUG.
XX
KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM detection; ss.
XX
OS Candida tropicalis.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PE 27-DEC-2000; 2000WO-DE04610.
XX
PF 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEFT A.
PA (STUE/) STUEBER F.
XX
PI Hoeft A, Stueber F;
XX
DR WPI: 2001-425677/45.
XX
PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides
XX
PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (1) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (II) from the physical properties of the (I)-ON complex, e.g.
CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the

CC invention.
XX
SQ Sequence 429 BP; 114 A; 85 C; 109 G; 119 T; 2 other;

Query Match 100.0%; Score 35; DB 22; Length 429;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
DB 380 CTAGTCGCATAGTTATGTTAAGACTACGACGG 346
|||||

RESULT 13
AAH21230/c
ID AAH21230 standard; DNA: 431 BP.
XX
AC AAH21230;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. albicans 16S rRNA DNA fragment YSASRSUA.
XX
KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM detection; ss.
XX
OS Candida albicans.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PE 27-DEC-2000; 2000WO-DE04610.
XX
PF 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEFT A.
PA (STUE/) STUEBER F.
XX
PI Hoeft A, Stueber F;
XX
DR WPI: 2001-425677/45.
XX
PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides
XX
PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (1) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (II) from the physical properties of the (I)-ON complex, e.g.
CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the
XX
SQ Sequence 431 BP; 115 A; 86 C; 110 G; 120 T; 0 other;

Query Match 100.0%; Score 35; DB 22; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35

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DB      382 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 348
      |||||||
RESULT 14
AAH21228/C
ID      AAH21228 standard; DNA: 432 BP.
XX
XX      AAH21228;
AC
XX      13-SEP-2001 (first entry)
DT
XX      C. parapsilosis 16S rRNA DNA fragment YSASRSUF.
DE
XX      Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM      food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM      detection; ss.
XX
XX      Candida parapsilosis.
OS
XX      WO200148237-A2.
PN
XX      05-JUL-2001.
PD
XX      27-DEC-2000; 2000WO-DE04610.
PF
XX      23-DEC-1999; 99DE-1062895.
PR      31-MAY-2000; 2000DE-1027113.
XX
PA      (HOEF/) HOEFT A.
PA      (STUE/) STUEBER F.
PI
XX      Hoeft A, Stueber F;
PI
XX      WPI: 2001-425677/45.
DR
XX      Rapid determination of microbial nucleic acid, useful e.g. for
PT      diagnosing bacterial infections, by analysis of temperature-dependent
PT      hybridization with oligonucleotides
XX
XX      Disclosure; Figure 13; 57pp; German.
XX
XX      This invention describes a novel method for detecting microbial DNA/RNA
CC      (I) by concentrating (I) from a sample, adding at least one labeled
CC      oligonucleotide (ON), performing temperature-dependent hybridization and
CC      determining (I) from the physical properties of the (I)-ON complex, e.g.
CC      the temperature dependence of hybridization. The method is used for rapid
CC      determination of microbial genomic RNA or DNA, particularly for diagnosis
CC      of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC      in intensive care patients), also for monitoring food and water, and for
CC      veterinary or forensic investigations. The method provides quick
CC      determination/identification of microbial nucleic acid. It is very
CC      sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC      represent primers and probes used to illustrate the method of the
CC      invention.
XX
XX      Sequence 432 BP; 114 A; 86 C; 110 G; 121 T; 1 other;
SQ
Query Match      100.0%; Score 35; DB 22; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
DB      383 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 349

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XX      13-SEP-2001 (first entry)
DT
XX      T. glabrata 16S rRNA DNA fragment YLSRSUA.
DE
XX      Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM      food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM      detection; ss.
XX
XX      Torulopsis glabrata.
OS
XX      WO200148237-A2.
PN
XX      05-JUL-2001.
PD
XX      27-DEC-2000; 2000WO-DE04610.
PF
XX      23-DEC-1999; 99DE-1062895.
PR      31-MAY-2000; 2000DE-1027113.
XX
PA      (HOEF/) HOEFT A.
PA      (STUE/) STUEBER F.
PI
XX      Hoeft A, Stueber F;
PI
XX      WPI: 2001-425677/45.
DR
XX      Rapid determination of microbial nucleic acid, useful e.g. for
PT      diagnosing bacterial infections, by analysis of temperature-dependent
PT      hybridization with oligonucleotides
XX
XX      Disclosure; Figure 13; 57pp; German.
XX
XX      This invention describes a novel method for detecting microbial DNA/RNA
CC      (I) by concentrating (I) from a sample, adding at least one labeled
CC      oligonucleotide (ON), performing temperature-dependent hybridization and
CC      determining (I) from the physical properties of the (I)-ON complex, e.g.
CC      the temperature dependence of hybridization. The method is used for rapid
CC      determination of microbial genomic RNA or DNA, particularly for diagnosis
CC      of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC      in intensive care patients), also for monitoring food and water, and for
CC      veterinary or forensic investigations. The method provides quick
CC      determination/identification of microbial nucleic acid. It is very
CC      sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC      represent primers and probes used to illustrate the method of the
CC      invention.
XX
XX      Sequence 444 BP; 115 A; 89 C; 117 G; 118 T; 5 other;
SQ
Query Match      100.0%; Score 35; DB 22; Length 444;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
DB      395 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 361

```

Search completed: August 6, 2003, 23:02:40
 Job time : 219.75 secs

```

RESULT 15
AAH21227/C
ID      AAH21227 standard; DNA: 444 BP.
XX
XX      AAH21227;
AC

```

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:26:11 ; Search time 856.953 Seconds

(without alignments)
1670.846 Million cell updates/sec

Title: US-09-846-797-6

Perfect score: 35

Sequence: 1 ctactgcgcacagttatggttaagactacgagc 35

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
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15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
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25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rnd: *
36: em_hlg_mam: *
37: em_hlg_vrt: *
38: em_gy: *
39: em_hlgo_hum: *
40: em_hlgo_mus: *
41: em_hlgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	35	100.0	35 6 AX298064	AX298064 Sequence
2	35	100.0	51 6 AR107728	AR107728 Sequence
3	35	100.0	51 6 AR107732	AR107732 Sequence
4	35	100.0	52 6 AR107725	AR107725 Sequence
5	35	100.0	52 6 AR107726	AR107726 Sequence
6	35	100.0	52 6 AR107727	AR107727 Sequence
7	35	100.0	52 6 AR107730	AR107730 Sequence
8	35	100.0	72 8 LC048426	U48426 Lenspora CO
9	35	100.0	75 6 AX406742	AX406742 Sequence
10	35	100.0	113 6 AX298065	AX298065 Sequence
11	35	100.0	113 6 AX298066	AX298066 Sequence
12	35	100.0	126 8 CA281374	Z81374 C.aeruginos
13	35	100.0	192 3 SARSSRB	M54960 S.giganthea
14	35	100.0	192 3 SARSSRB	X91535 Uncultured
15	35	100.0	261 3 S4172083	S4172083 small subun
16	35	100.0	261 3 S4172652	S4172652 small subun
17	35	100.0	266 8 EUSPUN4AB	Z69269 Uncultured
18	35	100.0	277 3 TOXRSS2	M17556 T.gondii sm
19	35	100.0	305 8 AF452625	AF452625 Glomus sp
20	35	100.0	311 8 AF213264	AF213264 Unculture
21	35	100.0	341 3 SN03148	U3148 Sarcocystis
22	35	100.0	346 8 AY150800	AY150800 Cladophia
23	35	100.0	346 8 MCUSUINB	AJ226070 Myrioscle
24	35	100.0	346 8 MCUSUINA	AJ226071 Myrioscle
25	35	100.0	347 8 MSCSSUNA	AJ226073 Myrioscle
26	35	100.0	347 8 MSCSSUNC	AJ226074 Myrioscle
27	35	100.0	347 8 MSCSSUND	AJ226075 Myrioscle
28	35	100.0	347 8 MSCSSUNE	AJ226076 Myrioscle
29	35	100.0	348 8 MDESSUINP	AJ226077 Myrioscle
30	35	100.0	364 3 AF424810	AF424810 Cryptospo
31	35	100.0	372 8 AY150799	AY150799 Cladophia
32	35	100.0	375 8 AY150798	AY150798 Cladophia
33	35	100.0	378 8 AF504732	AF504732 Unculture
34	35	100.0	379 8 AF504731	AF504731 Unculture
35	35	100.0	380 8 AF504734	AF504734 Unculture
36	35	100.0	381 8 AF247744	AF247744 Uncidentif
37	35	100.0	381 8 AF504733	AF504733 Unculture
38	35	100.0	382 8 AF504728	AF504728 Unculture
39	35	100.0	382 8 AF504729	AF504729 Unculture
40	35	100.0	384 8 EUSPS1	Z69305 Uncultured
41	35	100.0	385 8 AF504735	AF504735 Unculture
42	35	100.0	390 3 AY029361	AY029361 Cryptospo
43	35	100.0	394 8 AY055059	AY055059 Ascomycot
44	35	100.0	402 8 AF183384	AF183384 Unculture
45	35	100.0	402 8 AY035060	AY035060 Ascomycot

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AX298064	AX298064	Sequence 6 from Patent WO0183821.	AX298064	AX298064.1	GI:17128150		Candida albicans	1	Hogan, J.J. and Gordon, P.C.	Polynucleotide probes for detection and quantitation of Candida species
							Candida albicans			
							Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
							Saccharomycetales; mitosporic Saccharomycetales; Candida.			

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0183821-A 6 08-NOV-2001;
Gen-Probe Incorporated (US)
FEATURES
source
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/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
BASE COUNT 9 a 6 c 10 g 10 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGCGCATAGTTATGTTAGACTACGACGG 35
Db 1 CTAGTCGGCATAGTTATGTTAGACTACGACGG 35

RESULT 2
LOCUS ARI07728/c 51 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 81 from patent US 6110665.
ACCESSION ARI07728
VERSION ARI07728.1 GI:12823215
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadagnostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 81 29-AUG-2000;
FEATURES Location/Qualifiers
source 1. .51
/organism="unknown"

BASE COUNT 17 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGGCATAGTTATGTTAGACTACGACGG 35
Db 49 CTAGTCGGCATAGTTATGTTAGACTACGACGG 15

RESULT 3
LOCUS ARI07732/c 51 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 85 from patent US 6110665.
ACCESSION ARI07732
VERSION ARI07732.1 GI:12823219
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadagnostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 85 29-AUG-2000;
FEATURES Location/Qualifiers
source 1. .51
/organism="unknown"

BASE COUNT 17 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTACTCGCATAGTTATGTTAGACTACGACGG 35
Db 49 CTACTCGCATAGTTATGTTAGACTACGACGG 15

RESULT 4
LOCUS ARI07725/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 78 from patent US 6110665.
ACCESSION ARI07725
VERSION ARI07725.1 GI:12823212
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadagnostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 78 29-AUG-2000;
FEATURES Location/Qualifiers
source 1. .52
/organism="unknown"

BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTACTCGCATAGTTATGTTAGACTACGACGG 35
Db 50 CTACTCGCATAGTTATGTTAGACTACGACGG 16

RESULT 5
LOCUS ARI07726/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 79 from patent US 6110665.
ACCESSION ARI07726
VERSION ARI07726.1 GI:12823213
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadagnostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 79 29-AUG-2000;
FEATURES Location/Qualifiers
source 1. .52
/organism="unknown"

BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTACTCGCATAGTTATGTTAGACTACGACGG 35
Db 50 CTACTCGCATAGTTATGTTAGACTACGACGG 16

RESULT 6
LOCUS ARI07727/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 80 from patent US 6110665.
ACCESSION ARI07727
VERSION ARI07727.1 GI:12823214
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 52)
TITLE Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.
JOURNAL Sarcocystis neuroendoneuronal primer and its use in methods of
FEATURES equine protozoal myeloencephalitis diagnosis
Patent: US 6110665-A 80 29-AUG-2000;
Location/Qualifiers
1..52
Source /organism="unknown"
BASE COUNT 17 a 12 c 11 g 11 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
50 CTAGTCGGCATAGTTATGTTAAGACTACGACG 16

RESULT 7
LOCUS AR107730 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 83 from patent US 6110665.
ACCESSION AR107730
VERSION AR107730.1 GI:12823217
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.
TITLE Sarcocystis neuroendoneuronal primer and its use in methods of
JOURNAL equine protozoal myeloencephalitis diagnosis
FEATURES Patent: US 6110665-A 83 29-AUG-2000;
Location/Qualifiers
1..52
Source /organism="unknown"
BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTACTCGGCATAGTTATGTTAAGACTACGACG 35
50 CTAGTCGGCATAGTTATGTTAAGACTACGACG 16

RESULT 8
LOCUS LCU48426 72 bp DNA linear PLN 29-JUN-1996
DEFINITION Lanspora coronata nuclear-encoded small subunit ribosomal RNA gene,
ACCESSION U48426
VERSION U48426.1 GI:1399168
KEYWORDS
SOURCE Lanspora coronata
ORGANISM Lanspora coronata
REFERENCE Hypocremomyces; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Eukaryota; Fungi; Halosphaeriales; Halosphaeriaceae; Lanspora.
TITLE Spatafora, J.W., Volkman-Kohlmeier, B. and Kohlmeier, J.
JOURNAL Independent terrestrial origins of the Halosphaeriales (marine
REFERENCE Ascomycota)
AUTHORS unpublished
TITLE 2 (bases 1 to 72)
JOURNAL Spatafora, J.W., Volkman-Kohlmeier, B. and Kohlmeier, J.
REFERENCE Direct Submission

JOURNAL Submitted (02-FEB-1996) Joseph W. Spatafora, Botany & Plant
PATHOLOGY, Oregon State University, 2082 Cordley Hall, Corvallis,
OR 97331-2902, USA
FEATURES Location/Qualifiers
SOURCE 1..72
/organism="Lanspora coronata"
/mol_type="genomic DNA"
/strain="JK 4839A"
/db_xref="taxon:45830"
/note="from the culture collection of Jan and Brigitte
Kohlmeier (JK 4839A); amplified with primers NS1/NS4
(White et al., 1990) and sequenced with primers NS1, NS2,
NS4 (White et al., 1990), SR1R (Spatafora et al., 1995)
and SR7R (Vilgalys unpub.)."
complement(1..>72)
/product="small subunit ribosomal RNA"
BASE COUNT 18 a 16 c 15 g 23 t
ORIGIN

Query Match 100.0%; Score 35; DB 8; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
41 CTAGTCGGCATAGTTATGTTAAGACTACGACG 7

RESULT 9
LOCUS AX406742 75 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 6 from Patent WO0227021.
ACCESSION AX406742
VERSION AX406742.1 GI:21439667
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE Boettger, E.C., Rosenau, J., Kirschner, P. and Jack, T.
AUTHORS Method for detecting fungal infections
TITLE Patent: WO 0227021-A 6 04-APR-2002;
JOURNAL Cytomet GmbH & Co. KG (DE)
FEATURES Location/Qualifiers
SOURCE 1..75
/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
BASE COUNT 15 a 20 c 14 g 25 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTACTCGGCATAGTTATGTTAAGACTACGACG 35
8 CTAGTCGGCATAGTTATGTTAAGACTACGACG 42

RESULT 10
LOCUS AX298065 113 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 7 from Patent WO0183821.
ACCESSION AX298065
VERSION AX298065.1 GI:17128151
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS Saccharomycetales; mitosporic Saccharomycetales; Candida.

AUTHORS Hogan, J.J. and Gordon, P.C.
TITLE Polynucleotide probes for detection and quantitation of *Candida* species
JOURNAL Patent: WO 0183821-A 7 08-NOV-2001;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
SOURCE 1.113
/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
misc_structure 1.113
/note="Probe domain"
BASE COUNT 35 a 27 c 23 g 28 t
ORIGIN
Query Match 100.0%; Score 35; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
|||||
70 CTACTCGCATAGTTATGTTAAGACTACGACGG 104

RESULT 11
LOCUS AX298066 113 bp mRNA linear PAT 26-NOV-2001
DEFINITION Sequence 8 from Patent WO0183821.
ACCESSION AX298066
VERSION AX298066.1 GI:17128152
KEYWORDS
SOURCE
ORGANISM
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Hogan, J.J. and Gordon, P.C.
TITLE Polynucleotide probes for detection and quantitation of *Candida* species
JOURNAL Patent: WO 0183821-A 8 08-NOV-2001;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
SOURCE 1.113
/organism="Candida albicans"
/mol_type="mRNA"
/db_xref="taxon:5476"
misc_structure 1.113
/note="Sequence of rRNA target region"
BASE COUNT 28 a 23 c 27 g 35 t
ORIGIN
Query Match 100.0%; Score 35; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
|||||
44 CTAGTCGCATAGTTATGTTAAGACTACGACGG 10

RESULT 12
LOCUS CAZ81374 126 bp DNA linear PLN 22-JAN-1998
DEFINITION C. aeruginosa 18S rRNA gene.
ACCESSION Z81374
VERSION Z81374.1 GI:2808818
KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
SOURCE Chlorociboria aeruginosa
ORGANISM Chlorociboria aeruginosa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Helotiaceae; Chlorociboria.
REFERENCE 1 (bases 1 to 126)
AUTHORS Holst-Jensen, A.

TITLE Direct Submission
JOURNAL Submitted (29-OCT-1996) Holst-Jensen A., Division of Botany,
Department of Biology, University of Oslo, P.O. Box 1045, Blindern
0316, Oslo, NORWAY
FEATURES Location/Qualifiers
SOURCE 1.126
/organism="Chlorociboria aeruginosa"
/mol_type="genomic DNA"
/strain="1785.P on dead hardwood"
/db_xref="taxon:54693"
gene 1.126
/gene="18S rRNA"
rRNA <1.126
/gene="18S rRNA"
/product="18S ribosomal RNA"
BASE COUNT 30 a 26 c 34 g 36 t
ORIGIN
Query Match 100.0%; Score 35; DB 8; Length 126;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
|||||
41 CTAGTCGCATAGTTATGTTAAGACTACGACGG 7

RESULT 13
LOCUS SARSSRB/C 192 bp rRNA linear INV 27-APR-1993
DEFINITION S.giganthea small subunit ribosomal RNA.
ACCESSION M54960 M37052
VERSION M54960.1 GI:175888
KEYWORDS ribosomal RNA small subunit.
SOURCE Sarcocystis gigantea
ORGANISM Sarcocystis gigantea
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Sarcocystis.
REFERENCE 1 (bases 1 to 192)
AUTHORS Johnson, A.M., Irlana, S., Hakendorf, P. and Baverstock, P.R.
TITLE Phylogenetic relationships of the apicomplexan protist *Sarcocystis* as determined by small subunit ribosomal RNA comparison
JOURNAL J. Parasitol. 74 (5), 847-860 (1988)
MEDLINE 88332524
PUBMED 3138398
COMMENT Original source text: S.giganthea ribosomal RNA.
FEATURES Location/Qualifiers
SOURCE 1.192
/organism="Sarcocystis gigantea"
/mol_type="rRNA"
/db_xref="taxon:5814"
BASE COUNT 65 a 36 c 39 g 52 t
ORIGIN
Query Match 100.0%; Score 35; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
|||||
140 CTAGTCGCATAGTTATGTTAAGACTACGACGG 106

RESULT 14
LOCUS ESPX91535/C 217 bp DNA linear PLN 10-FEB-2003
DEFINITION Uncultured saccharomycete partial 18S rRNA gene (clone group K20).
ACCESSION X91535
VERSION X91535.1 GI:987810
KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
SOURCE uncultured saccharomycete
ORGANISM uncultured saccharomycete
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

unclassified Saccharomycetes; environmental samples.

REFERENCE 1 Pedersen, K.
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 217)
REFERENCE
AUTHORS Pedersen, K.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1995) K. Pedersen, Lundberg Institute, General
and Marine Microbiology, Medicinaregatan 9 E, 413 90 Goeteborg,
SWEDEN

FEATURES
source location/Qualifiers

1. 217
/organism="uncultured saccharomycete"
/mol_type="genomic DNA"
/isolation_source="Isolated from bentonite/sand buffer
material from the underground research laboratory at
AECL/Whiteshell laboratories"
/db_xref="taxon:212404"
/clone="clone group K20"
/environmental_sample
/country="Canada"
1. 217
/gene="18S rRNA"
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/gene="18S rRNA"
/product="18S ribosomal RNA"

BASE COUNT 65 a 36 c 55 g 61 t
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Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGGCATAGTTTATGTTAAGACTACGACGG 35
|||||
Db 200 CTAGTCGGCATAGTTTATGTTAAGACTACGACGG 166

RESULT 15
S41720S3/C 261 bp RNA linear INV 08-MAY-1993
LOCUS
DEFINITION small subunit rRNA (D/A-region and B-region) [Sarcocystis
capracanis, rRNA Partial, 261 nt, segment 3 of 3].

ACCESSION S41710
S41710.1 GI:252752

VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM

3 of 3
Sarcocystis capracanis
Sarcocystis capracanis
Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
Sarcocystidae; Sarcocystis.

REFERENCE 1 (bases 1 to 261)
AUTHORS Tenter, A.M., Baverstock, P.R. and Johnson, A.M.
TITLE Phylogenetic relationships of Sarcocystis species from sheep,
goats, cattle and mice based on ribosomal RNA sequences
JOURNAL Int. J. Parasitol. 22 (4), 503-513 (1992)
MEDLINE 92355206
PUBMED 1644525

REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI g1bdsq 110244] from the original journal article.
This sequence comes from Fig. 1C and 1D.
location/Qualifiers

FEATURES
source

1. 261
/organism="Sarcocystis capracanis"
/mol_type="rRNA"
/db_xref="taxon:5816"

gene order(S41720.1:1..210,join(S41716.1:1..61,1..261))
rRNA order(S41720.1:1..210,join(S41716.1:1..61,1..261))
/gene="small subunit rRNA"
/product="small subunit rRNA"

BASE COUNT 77 a 43 c 53 g 70 t 18 others
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Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGGCATAGTTTATGTTAAGACTACGACGG 35
|||||
Db 202 CTAGTCGGCATAGTTTATGTTAAGACTACGACGG 168

Search completed: August 6, 2003, 23:29:02
Job time : 858.953 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: August 6, 2003, 22:51:21 ; Search time 1568.72 seconds

(without alignments)
449.303 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 29

Sequence: 1 ggcgtcaataaagacacacacgaccc 29

Scoring table: IDENTITY_NUC

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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1: em_estda:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estor:
6: em_estpl:
7: em_estro:
8: em_estt:
9: gb_estl:
10: gb_estc:
11: gb_estc:
12: gb_estc:
13: gb_estc:
14: gb_estc:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inu:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rtd:
26: em_gss_pbg:
27: em_gss_vrt:
28: gb_gssl:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	29	100.0	615	10 BE337371 894045E04
C 2	29	100.0	943	29 CNS07CL7 AL439313 T7 end of
C 3	29	100.0	949	29 CNS07D7V AL440561 T3 end of
C 4	29	100.0	959	29 CNS07EBL AL441487 T7 end of

C 5	29	100.0	961	29 CNS07DW1 AL440999 T7 end of
C 6	29	100.0	966	29 CNS07E4J AL441305 T7 end of
C 7	29	100.0	971	29 CNS07DAJ AL442225 T7 end of
C 8	29	100.0	994	29 CNS07CJ3 AL438633 T7 end of
C 9	29	100.0	996	29 CNS07CCK AL438915 T7 end of
C 10	29	100.0	1010	29 CNS07CCK AL438915 T7 end of
C 11	29	100.0	1027	29 CNS07CRE AL441469 T3 end of
C 12	29	100.0	1029	29 CNS07DCK AL440599 T7 end of
C 13	29	100.0	1036	29 CNS07D77 AL440465 T7 end of
C 14	29	100.0	1038	29 CNS07C9I AL438892 T7 end of
C 15	29	100.0	1041	29 CNS07CNA AL438388 T3 end of
C 16	29	100.0	1066	29 CNS07DIY AL439916 T3 end of
C 17	29	100.0	1071	29 CNS07E4H AL441519 T7 end of
C 18	29	100.0	1120	29 CNS07EC4 AL441578 T3 end of
C 19	28.6	98.6	980	29 CNS07CEX AL438087 T7 end of
C 20	27.4	94.5	997	29 CNS07DQ1 AL440783 T7 end of
C 21	25.8	89.0	888	29 CNS06VOP AL4417623 T3 end of
C 22	25.8	89.0	889	29 CNS06W2D AL4419087 T3 end of
C 23	25.8	89.0	928	29 CNS06V38 AL441634 T7 end of
C 24	25.8	89.0	934	29 CNS06V72 AL4417564 T3 end of
C 25	25.8	89.0	941	29 CNS06X3M AL4419240 T7 end of
C 26	25.8	89.0	944	29 CNS06X1I AL4419164 T7 end of
C 27	25.8	89.0	949	29 CNS07B5Y AL437468 T7 end of
C 28	25.8	89.0	958	29 CNS06BEM AL4418232 T3 end of
C 29	25.8	89.0	1034	29 CNS07BAS1 AL436984 T7 end of
C 30	25.4	87.6	1077	29 CNS07B2A AL437336 T3 end of
C 31	25.4	87.6	906	29 CNS06X7U AL419680 T3 end of
C 32	24.8	85.5	809	29 CNS06WUP AL418523 T3 end of
C 33	24.8	85.5	927	29 CNS07A54 AL436142 T7 end of
C 34	23.2	80.0	854	13 BU180498 AGENCOURT B2301816
C 35	22.6	77.9	502	29 B2301816 B2301816
C 36	22.6	77.9	524	29 B2305052 KD3296.p1
C 37	21.8	75.2	710	29 CNS07BRJ AL438245 T7 end of
C 38	21	72.4	224	28 A2931573 474.dh286
C 39	21	72.4	292	28 A2124549 b107r.S.
C 40	21	72.4	381	28 A2931738 474.dh289
C 41	21	72.4	438	28 A2929878 479.d1156
C 42	21	72.4	440	28 A2930332 474.dh253
C 43	21	72.4	459	29 CNS06X7K AL420174 T3 end of
C 44	21	72.4	467	28 A2929872 479.d1136
C 45	21	72.4	473	29 CNS06XTD AL420167 T7 end of

ALIGNMENTS

RESULT 1
BE337371 615 bp mRNA linear EST 14-Jul-2000
LOCUS 894045E04.x1 C. reinhardtii CC-1690, normalized, Lambda zap II
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BE337371
VERSION BE337371.1 GI:9210456
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii

REFERENCE 1 (bases 1 to 615)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
Modermott, J. P., Sillflow, C., Stern, P. and Surryck, R.

TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
JOURNAL Unicellular System for Analyzing Gene Function and Regulation in
COMMENT Unpublished
Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University,
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers

FEATURES

source

1. .615
 /organism="Chlamydomonas reinhardtii"
 /mol_type="mRNA"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_11b="C. reinhardtii CC-1690, normalized, Lambda Zap II"
 /note="Vector: Bluescript II SK-, Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in YAP (acetate-containing) medium in the light, YAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into Lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. Bluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1995) Genome Research 6: 791-806."

BASE COUNT 169 a 104 c 163 g 179 t
 ORIGIN

Query Match 100.0%; Score 29; DB 10; Length 615;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCAATTAAGACACACACCGATCCC 29
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 Db 277 GCCTCAATTAAGACACACACCGATCCC 249

RESULT 2
 CENS07CL7 943 bp DNA linear GSS 08-JUL-2001
 LOCUS T7 end of clone BD0AA003G09 of library BD0A from strain CBS 94 of
 DEFINITION Candida tropicalis, genomic survey sequence.
 ACCESSION AL439313
 VERSION AL439313.1 GI:12222726
 KEYWORDS GSS.
 SOURCE Candida tropicalis
 ORGANISM Candida tropicalis

REFERENCE
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neugeilise,C., Ozler-Kalogeropoulos,O., Potter,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 1 (bases 1 to 943)
 Saccharomycetales; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

TITLE
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876

REFERENCE
 AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and Dujon,B.
 2 (bases 1 to 943)
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

TITLE
 JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
 MEDLINE 20584726
 PUBMED 11152891
 REFERENCE 3 (bases 1 to 943)
 TITLE Genoscope.
 AUTHORS Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segref@genoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source
 1. .943
 /organism="Candida tropicalis"
 /mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
 /clone_11b="BD0AA003G09"
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 /note="end : T7"
 <1. >943
 /note="part of rDNA repeats
 contains 35S rDNA"
 /evidence=not_experimental

BASE COUNT 249 a 173 c 242 g 269 t 10 others
 ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 943;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCAATTAAGACACACACCGATCCC 29
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 Db 597 GCCTCAATTAAGACACACACCGATCCC 569

RESULT 3
 CENS07DJV 949 bp DNA linear GSS 08-JUL-2001
 LOCUS T3 end of clone BD0AA013C01 of library BD0A from strain CBS 94 of
 DEFINITION Candida tropicalis, genomic survey sequence.
 ACCESSION AL440561
 VERSION AL440561.1 GI:12223972
 KEYWORDS GSS.
 SOURCE Candida tropicalis
 ORGANISM Candida tropicalis

REFERENCE
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neugeilise,C., Ozler-Kalogeropoulos,O., Potter,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 1 (bases 1 to 949)
 Saccharomycetales; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

TITLE
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876

REFERENCE
 AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and Dujon,B.
 2 (bases 1 to 949)
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

TITLE
 JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
 MEDLINE 20584726
 PUBMED 11152891
 REFERENCE 3 (bases 1 to 949)
 TITLE Genoscope.
 AUTHORS Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segref@genoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..949
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0AA013C01"
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/note="end : T3"
<1..>949
/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not-experimental

BASE COUNT 251 a 179 c 260 g 253 t 6 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 949;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGACACACACCGATCCC 29
Db 213 GCCTCATTAAGACACACACCGATCCC 185

RESULT 4
LOCUS CNS07E9L 959 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone XBD0AA002C12 of library XBD0AA from strain CBS 94
ACCESSION AL441487
VERSION AL441487.1 GI:12224713
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
de Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 959)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 959)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..959
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="XBD0AA002C12"
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/note="end : T7"
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/note="part of rDNA repeats
contains 18S rDNA"
/evidence=not-experimental

BASE COUNT 267 a 188 c 249 g 252 t 3 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 959;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGACACACACCGATCCC 29
Db 794 GCCTCATTAAGACACACACCGATCCC 766

RESULT 5
LOCUS CNS07DW1L 961 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0AA016B05 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
ACCESSION AL440999
VERSION AL440999.1 GI:12224407
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
de Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 961)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 961)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

location/Qualifiers
1..961
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/mol_type="genomic DNA"
/strain="CBS 94"
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/clone_1lb="BD0A"
/note="end : T7"
<1..>961
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 252 a 182 c 256 g 268 t 3 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 961;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCATTAAGACACACACCGATCC 29
Db 502 GCCTCATTAAGACACACACCGATCC 474

RESULT 6
CNS07E4J/c 966 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone XBD0A01A07 of library XBD0A from strain CBS 94
DEFINITION of *Candida tropicalis*, genomic survey sequence.
ACCESSION AL441305
VERSION AL441305.1 GI:12224531
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM *Candida tropicalis*
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 966)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 966)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. *Candida*
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 966)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

location/Qualifiers
1..966
/organism="Candida tropicalis"
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/strain="CBS 94"
/db_xref="taxon:5482"
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/note="end : T7"
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/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 243 a 190 c 240 g 274 t 19 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 966;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCATTAAGACACACACCGATCC 29
Db 85 GCCTCATTAAGACACACACCGATCC 57

RESULT 7
CNS07DAJ/c 971 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0A010H04 of library BD0A from strain CBS 94 of
DEFINITION *Candida tropicalis*, genomic survey sequence.
ACCESSION AL440225
VERSION AL440225.1 GI:12223636
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM *Candida tropicalis*
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 971)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 971)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. *Candida*
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 971)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

COMMENT

This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

Location/Qualifiers
1..971
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A010H04"
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/note="end : T7"
<1..>971
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 253 a 188 c 252 g 272 t 6 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 971;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCATTAAGACACACACCGATCCC 29
Db 374 GCGTCATTAAGACACACACCGATCCC 346

RESULT 8
LOCUS CNS07CU3 994 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0A006H01 of library BD0A from strain CBS 94 of
ACCESSION AL439633
VERSION AL439633.1 GI:12223046
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 994)
Biolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neveuglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 994)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*.

COMMENT

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

Location/Qualifiers
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/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A006H01"
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/note="end : T7"
<1..>994
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 283 a 263 c 189 g 258 t 1 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCATTAAGACACACACCGATCCC 29
Db 502 GCGTCATTAAGACACACACCGATCCC 530

RESULT 9
LOCUS CNS07CCX 996 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0A001H09 of library BD0A from strain CBS 94 of
ACCESSION AL439015
VERSION AL439015.1 GI:12222428
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 996)
Biolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neveuglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

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yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 996)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*.

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

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contains 18S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 268 a 256 c 192 g 278 t 2 others
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Query Match 100.0%; Score 29; DB 29; Length 996;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACCGATCCC 29
Db 191 GCCTCATTAAGAACACACCGATCCC 219

RESULT 10
CNS07CRE 1010 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone BD0A006B09 of library BD0AA from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL439536
VERSION AL439536.1 GI:12222949
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1010)
Soclet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lorente, B.,
Malpertuy, A., Neveuglise, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 1010)
Blandin, G., Ozler-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
Dujon, B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 1010)
JOURNAL Direct Submission
TITLES Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1010
/organism="Candida tropicalis"
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/db_xref="taxon:5482"
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contains 35S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 266 a 201 c 258 g 284 t 1 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1010;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACCGATCCC 29
Db 38 GCCTCATTAAGAACACACCGATCCC 10

RESULT 11
CNS07E90 1027 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone XBD0A002C01 of library XBD0AA from strain CBS 94
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL441466
VERSION AL441466.1 GI:12224692
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1027)
Soclet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lorente, B.,
Malpertuy, A., Neveuglise, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 1027)
Blandin, G., Ozler-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
Dujon, B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 1027)
JOURNAL Direct Submission
TITLES Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

COMMENT

COMMENT

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1027
/organism="Candida tropicalis"
/mol_type="genomic DNA"
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/db_xref="taxon:5482"
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contains 18S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 287 a 195 c 264 g 279 t 2 others
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Query Match 100.0%; Score 29; DB 29; Length 1027;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAAGACACACACCGATCCC 29
Db 879 GCGTCATATAAAGACACACACCGATCCC 851

RESULT 12
CNS07DKX/c 1029 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0AA013E02 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440599
VERSION AL440599.1 GI:12224010
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 1029)
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711

REFERENCE
AUTHORS 2 (bases 1 to 1029)
Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726

REFERENCE
AUTHORS 3 (bases 1 to 1029)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

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/mol_type="genomic DNA"
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/db_xref="taxon:5482"
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/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 261 a 216 c 272 g 277 t 3 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAAGACACACACCGATCCC 29
Db 111 GCGTCATATAAAGACACACACCGATCCC 83

RESULT 13
CNS07DH7/c 1036 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0AA012E03 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440465
VERSION AL440465.1 GI:12223876
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 1036)
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711

REFERENCE
AUTHORS 2 (bases 1 to 1036)
Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726

REFERENCE
AUTHORS 3 (bases 1 to 1036)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

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/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A012F03"
/clone_1lb="BD0A"
/note="end : T7"
<1..>1036
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

BASE COUNT 272 a 194 c 276 g 291 t 3 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
Db 269 GCCTCAATAAAGACACACACCGATCCC 241

RESULT 14
CNS07C91 1038 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0A001A11 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL438892
VERSION AL438892.1 GI:12222305
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
AUTHORS Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
AUTHORS Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis

JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 1038)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..1038
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A001A11"
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/note="end : T7"
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/note="part of rDNA repeats
contains 18S rDNA"
/evidence="not-experimental"

BASE COUNT 281 a 265 c 197 g 291 t 4 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1038;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
Db 200 GCCTCAATAAAGACACACACCGATCCC 228

RESULT 15
CNS07CNA 1041 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone BD0A004C06 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL439388
VERSION AL439388.1 GI:12222801
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
AUTHORS Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
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yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
AUTHORS Dujon,B.
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tropicalis

JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 1041)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
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segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
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exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1041
 location/Qualifiers
 /organism="Candida tropicalis"
 /mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
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 /clone_1lb="BD0A"
 /note="end : T3"
 <1..>1041
 /note="part of rDNA repeats
 contains 35S rDNA"
 /evidence="not_experimental"

misc_feature

BASE COUNT 287 a 272 c 198 g 282 t 2 others
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 29; DB 29; Length 1041;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GCGTCATTAAGAACAACGATCCC 29
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Db

414 GCGTCATTAAGAACAACGATCCC 442

Search completed: August 7, 2003, 00:28:26
 Job time : 1570.72 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 22:54:01 ; Search time 112.375 Seconds

(without alignments)
532.387 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 1 gcgcataaagaagacaacacgaccc 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : .published.Applications_NA.*

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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PTCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.2	66.2	585	US-10-027-632-288539	Sequence 288539, AP
C 2	19	65.5	945	US-09-938-842A-5257	Sequence 5257, AP
C 3	18.6	64.1	9091	US-10-239-676-82	Sequence 82, Appl
C 4	18	62.1	491	US-10-027-632-46818	Sequence 46818, A
C 5	18	62.1	491	US-10-027-632-46819	Sequence 46819, A
C 6	18	62.1	508	US-10-027-632-77880	Sequence 77880, A
C 7	18	62.1	508	US-10-027-632-77881	Sequence 77881, A
C 8	18	62.1	508	US-10-027-632-314241	Sequence 314241, A
C 9	18	62.1	508	US-10-027-632-314242	Sequence 314242, A
C 10	18	62.1	9246	US-10-265-891-25	Sequence 25, Appl
C 11	18	62.1	32167	US-09-764-891-8197	Sequence 8197, AP
C 12	17.8	61.4	567	US-10-027-632-89343	Sequence 89343, A
C 13	17.8	61.4	567	US-10-027-632-303956	Sequence 303956, A
C 14	17.8	61.4	634	US-09-560-863-832	Sequence 832, AP
C 15	17.8	61.4	655	US-10-027-632-216183	Sequence 216183, AP
C 16	17.8	61.4	1605	US-09-938-842A-2031	Sequence 2031, AP

17	17.8	61.4	3119	US-10-002-600-70	Sequence 70, Appl
C 18	17.8	61.4	7038	US-10-239-676-204	Sequence 204, AP
C 19	17.6	60.7	463	US-10-198-846-87	Sequence 87, Appl
C 20	17.6	60.7	650	US-10-198-846-100310	Sequence 100310, A
C 21	17.6	60.7	653	US-10-198-846-7690	Sequence 7690, AP
C 22	17.6	60.7	3813	US-10-245-802-15	Sequence 15, Appl
C 23	17.6	60.7	5687	US-10-239-676-22	Sequence 22, Appl
C 24	17.6	60.7	7380	US-10-239-676-65	Sequence 65, Appl
C 25	17.6	60.7	7808	US-10-114-170-247	Sequence 247, AP
C 26	17.6	60.7	8693	US-10-172-086-38	Sequence 38, Appl
C 27	17.6	60.7	3186778	US-10-027-632-17961	Sequence 17961, AP
C 28	17.4	60.0	408	US-09-960-352-1398	Sequence 1398, AP
C 29	17.4	60.0	505	US-09-783-590-7723	Sequence 7723, AP
C 30	17.4	60.0	815	US-10-027-632-8065	Sequence 8065, AP
C 31	17.4	60.0	955	US-10-027-632-120370	Sequence 120370, A
C 32	17.2	59.3	423	US-10-027-632-133845	Sequence 133845, A
C 33	17.2	59.3	423	US-10-027-632-133846	Sequence 133846, A
C 34	17.2	59.3	640	US-10-027-632-102497	Sequence 102497, A
C 35	17.2	59.3	728	US-10-027-632-146117	Sequence 146117, A
C 36	17.2	59.3	1311	US-09-815-242-4178	Sequence 4178, AP
C 37	17.2	59.3	1347	US-09-815-242-8476	Sequence 8476, AP
C 38	17.2	59.3	1450	US-08-781-986A-280	Sequence 280, AP
C 39	17.2	59.3	1816	US-08-781-986A-351	Sequence 351, AP
C 40	17.2	59.3	2000	US-09-938-842A-3106	Sequence 3106, AP
C 41	17.2	59.3	2606	US-09-837-654-7	Sequence 7, Appl1
C 42	17.2	59.3	2606	US-09-837-654-7	Sequence 7, Appl1
C 43	17.2	59.3	3439	US-09-837-654-6	Sequence 6, Appl1
C 44	17.2	59.3	3439	US-09-837-654-6	Sequence 6, Appl1
C 45	17.2	59.3	6845	US-09-764-877-2124	Sequence 2124, AP

ALIGNMENTS

```
RESULT 1
US-10-027-632-288539/c
Sequence 288539, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wand, David G.
TITLE OR INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218, 006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185, 218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167, 363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156, 358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146, 002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 288539
LENGTH: 585
TYPE: DNA
ORGANISM: Human
US-10-027-632-288539
Query Match 66.2% Score 19.2; DB 13; Length 585;
Best Local Similarity 87.5%; Pred. No. 2e+02; 3; Indels 0;
Matches 21; Conservative 0; Mismatches 3; Gaps 0;
```

```
RESULT 2
US-09-938-842A-5257
; Sequence 5257, Application US/0938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5257
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5257

Query Match
Best Local Similarity 81.5%; Score 19; DB 10; Length 945;
Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGACAAACACCGATC 27
DB 155 GCATCAACATAGACAAACATGTAAC 181

RESULT 3
US-10-239-676-82/c
; Sequence 82, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239, 676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 82
; LENGTH: 9091
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-239-676-82

Query Match
Best Local Similarity 64.1%; Score 18.6; DB 14; Length 9091;
Pred. No. 5.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 5 CAATTAAGACAAACACCGATCCC 29
DB 1825 CAATTAAGACAAACACCGATCCC 1801

RESULT 4
US-10-027-632-46818
; Sequence 46818, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46818
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46818

Query Match
Best Local Similarity 80.8%; Score 18; DB 13; Length 491;
Pred. No. 5.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 TCATTAAGACAAACACCGATCCC 29
DB 129 TCATTAAGACAAACACCGATCCC 154

RESULT 5
US-10-027-632-46819
; Sequence 46819, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46819
```

```

; LENGTH: 491
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46819

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 491;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
    ||| |||| |||| |||| ||||
DB 129 TCATCAAGACACACAGGATCCC 154

RESULT 5
US-10-027-632-77880
; Sequence 77880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77880
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-77880

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
    ||| |||| |||| |||| ||||
DB 129 TCATCAAGACACACAGGATCCC 154

RESULT 7
US-10-027-632-77881
; Sequence 77881, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77881
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-77881

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
    ||| |||| |||| |||| ||||
DB 129 TCATCAAGACACACAGGATCCC 154

RESULT 8
US-10-027-632-314241
; Sequence 314241, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314241
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314241

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
    ||| |||| |||| |||| ||||
DB 129 TCATCAAGACACACAGGATCCC 154

RESULT 9
US-10-027-632-314242
; Sequence 314242, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314242
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314242
```

```

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Pred. No. 5.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```

Qy 4 TCATAAAGACACACACCGATCCC 29
Db 129 TCATTCAGACACACACCGATCCC 154
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```

RESULT 10
US-10-265-689-25/c
; Sequence 25, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURMIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9246
; TYPE: DNA
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
US-10-265-689-25
```

```

Query Match
Best Local Similarity 62.1%; Score 18; DB 14; Length 9246;
Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

Qy 1 GCGTCAATAAAGACACACCGAT 26
Db 2501 GAGCGAATAAATAAAGACACACCGAT 2476
```

RESULT 11

```

US-09-764-891-8197
; Sequence 8197, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8197
; LENGTH: 32167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8197
```

```

Query Match
Best Local Similarity 62.1%; Score 18; DB 11; Length 32167;
Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 4 TCATAAAGACACACACCGATCCC 29
Db 20304 TCAGTAAGAGAAAACACACCGATCCC 20329
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```

RESULT 12
US-10-027-632-89343/c
; Sequence 89343, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89343
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-89343
```

```

Query Match
Best Local Similarity 61.4%; Score 17.8; DB 13; Length 567;
Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

Qy 6 AATAAAGACACACACCGAT 26
Db 389 AATAAAGACACACACTGCT 369
```

```

RESULT 13
US-10-027-632-303956/c
; Sequence 303956, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303956
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-303956
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```

Query Match          61.4%; Score 17.8; DB 13; Length 567;
Best Local Similarity 90.5%; Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      6 AATTAAGACACACACGAT 26
      |||||
Db      389 AATTAAGACACACACTGCT 369

RESULT 14
US-09-560-863-832/C
; Sequence 832, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1 Human Polynucleotides and the
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 832
; LENGTH: 634
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(634)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-832
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Query Match          61.4%; Score 17.8; DB 10; Length 634;
Best Local Similarity 86.4%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      8 TAAAGACACACACGATCC 29
      |||||
Db      558 TAAAGACACACACGATCNC 537
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RESULT 15

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US-10-027-632-216183
; Sequence 216183, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216183
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(655)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-216183
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Query Match          61.4%; Score 17.8; DB 13; Length 655;
Best Local Similarity 90.5%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY      6 AATTAAGACACACACGAT 26
      |||||
Db      352 AATTAAGACACACACAGAT 372
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Search completed: August 7, 2003, 00:32:48
Job time : 115.375 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:25:31 ; Search time 181.25 Seconds

(without alignments)
431.910 Million cell updates/sec

Title: US-09-846-797-1

Sequence: 1 gcgtcaataaagacacacacgaccc 29

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	21	AAC81651
2	29	100.0	29	24	AAI70909
3	29	100.0	113	24	AAI70915
C 4	29	100.0	113	24	AAI70916
C 5	29	100.0	429	22	AAH21239
C 6	29	100.0	431	22	AAH21230
C 7	29	100.0	432	22	AAH21228
8	28	96.6	28	24	AAI70913

C 9	21	72.4	1776	22	AAF25849
C 10	21	72.4	1802	22	AAF23018
C 11	21	72.4	3420	24	ABAG9033
C 12	20.2	69.7	568	23	ABV50391
C 13	20	69.0	1078	24	ABO49302
C 14	20	69.0	1078	24	ABO49303
C 15	20	69.0	1080	24	ABO22352
C 16	20	69.0	1080	24	ABO22353
C 17	19.8	68.3	444	22	AAH21227
C 18	19.8	68.3	2307	22	AAH21227
C 19	19.8	68.3	2307	24	AB231771
C 20	19.8	68.3	4841	16	AAH05696
C 21	19.8	68.3	910715	20	AAH20248
C 22	19.6	67.6	747	24	ABO41242
C 23	19.6	67.6	747	24	ABO41243
C 24	19.6	67.6	2707	22	ABL29712
C 25	19.6	67.6	7497	22	AAH46638
C 26	19.6	67.6	7497	24	ABN80251
C 27	19.6	67.6	16545	24	ABL22050
C 28	19.4	66.9	2663	23	ABL24658
C 29	19.4	66.9	2968	23	ABL11176
C 30	19.2	66.2	526	24	ABO19854
C 31	19.2	66.2	526	24	ABO19855
C 32	19.2	66.2	8605	24	ABL32534
C 33	19	65.3	945	24	ABL217452
C 34	19	65.5	1798	22	AAH14004
C 35	19	65.5	1798	22	AAH14297
C 36	19	65.5	5319	23	ABL05960
C 37	18.8	64.8	3523	25	ABL10024
C 38	18.8	64.8	6523	24	ABN80121
C 39	18.8	64.8	10020	24	ABL54293
C 40	18.6	64.1	1133	24	ABO49444
C 41	18.6	64.1	1133	24	ABO49445
C 42	18.6	64.1	2204	18	AAH84019
C 43	18.6	64.1	5300	24	ABK39946
C 44	18.6	64.1	5300	24	ABL22548
C 45	18.6	64.1	6160	24	ABL70233

ALIGNMENTS

RESULT 1	
AAC81651	
ID	AAC81651 standard; DNA; 29 BP.
AC	AAC81651;
XX	
DT	09-MAR-2001 (first entry)
XX	
DE	Candida sp. rRNA/rDNA hybridisation probe, SEQ ID NO:55.
XX	
XX	
KW	Ribosomal nucleic acid; rRNA; rDNA; microorganism identification;
KW	bacterium; fungus; infection; clinical sample; diagnosis;
KW	nucleic acid matrix; nucleotide array; hybridisation probe; ss.
XX	
OS	Candida albicans.
OS	Candida tropicalis.
OS	Candida dubliniensis.
OS	Candida viswanathii.
XX	Candida parapsilosis.
XX	
PN	WO200066789-A2.
XX	
PD	09-NOV-2000.
XX	
PF	03-MAY-2000; 2000MO-US12421.
XX	
PR	03-MAY-1999; 99US-0132411.
XX	20-AUG-1999; 99US-0150149.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	

S. exiguus 18S rRNA
Yeast 18S rRNA seq
Saccharomyces cere
Human prostate exp
Oligonucleotide fo
Oligonucleotide fo
Oligonucleotide fo
Oligonucleotide fo
T. glabrata 16S rR
Candida albicans e
Candida albicans e
Plax rust resistan
Borrelia burgdorfe
Oligonucleotide fo
Oligonucleotide fo
Tumour suppressor
Human chemically m
Human immune syste
Drosophila melanog
Drosophila melanog
Oligonucleotide fo
Oligonucleotide fo
Human immune syste
Arabidopsis thaliana
DNA to infer yeast
Yeast DNA to infer
Hemophilic melanog
Human chemically cel
Human immune syste
Oligonucleotide fo
Oligonucleotide fo
DNA encoding a Sta
Human chemically p
Human immune syste
Chemically treated

PI Hogan JT;
 XX
 DR WPI; 2000-687550/67.
 XX
 PT A device for hybridizing nucleic acids useful for identifying
 PT microorganisms comprises a solid support and several addresses
 PT comprising a probe, disposed on the solid support -
 XX
 PS Disclosure; Page 40; 96pp; English.
 XX
 CC The invention relates to a nucleotide matrix for the identification
 CC of microorganisms, and a method of identifying the microorganisms(s)
 CC in a biological sample using the nucleotide matrix. The matrix comprises
 CC a collection of nucleic acid hybridisation probes, with each probe being
 CC specific for the ribosomal nucleic acids (rRNA or rDNA) of at least one
 CC microorganism (e.g., a bacterium or a fungus). The collection of probes
 CC is organised into a series of "addresses" that provide information about
 CC the presence or absence of one or more nucleotide sequences in the
 CC biological sample. Probes in the matrix are selected to distinguish
 CC between organisms that differ from each other by a known phylogenetic
 CC relationship. The addresses include a higher order address (the least
 CC organism-specific address which is able to bind to a ribosomal nucleic
 CC acid from a broad class of organisms e.g., one common to all fungi), an
 CC intermediate address and a lower order address (the most organism-
 CC specific). The lower order address hybridises rRNA/rDNA from a subset of
 CC organisms whose ribosomal nucleic acids hybridise to the intermediate
 CC order address. Likewise, the intermediate order address hybridises
 CC ribosomal nucleic acids from a subset of organisms having ribosomal
 CC nucleic acids that hybridise at the higher order address. The method and
 CC nucleic acid matrix of the invention is used for identifying
 CC microorganisms, especially in clinical samples. The method can detect
 CC and resolve the identities of microorganisms that are present in a mixed
 CC sample. The system is suited to automated analysis, and enables the
 CC identification of a disease-causing microorganism without the need for
 CC experienced technicians. The present sequence represents a ribosomal
 CC nucleic acid-specific hybridisation probe for use in a nucleic acid
 CC matrix of the invention.
 CC
 SQ Sequence 29 BP; 13 A; 9 C; 4 G; 3 T; 0 other;
 XX

Query Match 100.0%; Score 29; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGAAGACACACACCGATCCC 29
 ||||||||||||||||||||||||||||
 DB 1 GCGTCATTAAGAAGACACACACCGATCCC 29

RESULT 2
 AA170909
 ID AA170909 standard; DNA; 29 BP.
 XX
 AC AA170909;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Probe CALA1037 for Candida species detection and quantitation.
 XX
 KW Candida albicans; Candida tropicalis; Candida dubliniensis;
 KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
 XX
 OS Candida albicans.
 XX
 PN WO200183821-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 01-MAY-2001; 2001WO-US13884.
 XX
 PR 01-MAY-2000; 2000US-201249P.
 XX
 PA (GENP-) GEN-PROBE INC.

XX Hogan JT, Gordon PC;
 XX
 DR WPI; 2002-066537/09.
 XX
 PT Novel oligonucleotide sequences that are fully complementary to
 PT ribosomal RNA or DNA of Candida species, useful for detecting presence
 PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
 PT sample -
 XX
 PS Claim 2; Page 19; 33pp; English.
 XX
 CC The present sequence is that of oligonucleotide probe CALA1037,
 CC which is complementary to a unique segment (see AA170916) of the
 CC 18S ribosomal RNA of Candida albicans, Candida tropicalis, Candida
 CC dubliniensis, Candida viswanathii and Candida tropicalis. The
 CC probe is highly specific, and can distinguish these Candida species
 CC from their known phylogenetically nearest neighbours. It is
 CC useful for their detection and quantitation. Probe CALA1037 is
 CC 29 bases in length, has a Tm of 59.5 degree C, and hybridises rRNA
 CC in a manner that is enhanced by the presence of helper
 CC oligonucleotides (see AA170910-12). The probe is an illustration of
 CC an oligonucleotide that: (1) hybridises the target nucleic acid under
 CC high stringency hybridisation conditions; (2) has a length of up to
 CC 100 nucleotide bases; and (3) includes at least 15 contiguous
 CC nucleotides falling within the sequence given in AA170915 or its
 CC complement. It may include a detectable moiety, such as an
 CC acridinium ester or a radioisotope.
 CC
 SQ Sequence 29 BP; 13 A; 9 C; 4 G; 3 T; 0 other;
 XX

Query Match 100.0%; Score 29; DB 24; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGAAGACACACACCGATCCC 29
 ||||||||||||||||||||||||||||
 DB 1 GCGTCATTAAGAAGACACACACCGATCCC 29

RESULT 3
 AA170915
 ID AA170915 standard; DNA; 113 BP.
 XX
 AC AA170915;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Candida species 18S ribosomal DNA probe domain.
 XX
 KW Candida albicans; Candida tropicalis; Candida dubliniensis;
 KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
 XX
 OS Candida albicans.
 XX
 PN WO200183821-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 01-MAY-2001; 2001WO-US13884.
 XX
 PR 01-MAY-2000; 2000US-201249P.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Hogan JT, Gordon PC;
 XX
 DR WPI; 2002-066537/09.
 XX
 PT Novel oligonucleotide sequences that are fully complementary to
 PT ribosomal RNA or DNA of Candida species, useful for detecting presence
 PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
 PT sample -

XX Claim 1; Page 32; 33pp; English.

PS The present sequence is that of DNA corresponding to a unique
 CC segment (see AA170916) of the 18S ribosomal RNA of *Candida albicans*,
 CC *Candida tropicalis*, *Candida dubliniensis*, *Candida viswanathii* and
 CC *Candida tropicalis*. Claimed hybridisation probes and helper
 CC oligonucleotides (see AA170909-14) correspond to a portion of this
 CC sequence or its complement. The probes are highly specific, and can
 CC distinguish *Candida* species from their known phylogenetically
 CC nearest neighbours. They are useful for detection and quantitation.
 XX

SO Sequence 113 BP; 35 A; 27 C; 23 G; 28 T; 0 other;

Query Match 100.0%; Score 29; DB 24; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAATAAGAACACACCGATCCC 29
 DB 42 GCGTCATTAATAAGAACACACCGATCCC 70

RESULT 4

AA170916/C
 ID AA170916 standard; rRNA; 113 BP.

AC AA170916;

DT 12-MAR-2002 (first entry)

DE *Candida species* 18S ribosomal RNA probe domain.

KW *Candida albicans*; *Candida tropicalis*; *Candida dubliniensis*;

XX *Candida viswanathii*; *Candida parapsilosis*; detection; probe; ss.

OS *Candida albicans*.

PN WO200183821-A2.

PD 08-NOV-2001.

PF 01-MAY-2001; 2001WO-US13884.

PR 01-MAY-2000; 2000US-201249P.

PA (GENP-) GEN-PROBE INC.

XX Hogan JJ, Gordon PC;

PI Hogan JJ, Gordon PC;

DR WPI; 2002-066537/09.

PT Novel oligonucleotide sequences that are fully complementary to

PT ribosomal RNA or DNA of *Candida species*, useful for detecting presence

PT of *C. albicans*, *C. dubliniensis*, *C. viswanathii*, *C. parapsilosis* in test

PS sample.

XX Disclosure: Page 32; 33pp; English.

XX The present sequence is that of a unique segment of the 18S

CC ribosomal RNA of *Candida albicans*, *Candida tropicalis*,

CC *Candida dubliniensis*, *Candida viswanathii* and *Candida tropicalis*.

CC Claimed hybridisation probes and helper oligonucleotides (see

CC AA170909-14) correspond to a portion of this sequence or its

CC complement. The probes are highly specific, and can distinguish

CC these *Candida species* from their known phylogenetically nearest

XX neighbours. They are useful for detection and quantitation.

SO Sequence 113 BP; 28 A; 23 C; 27 G; 35 U; 0 other;

Query Match 100.0%; Score 29; DB 24; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAATAAGAACACACCGATCCC 29
 DB 72 GCGTCATTAATAAGAACACACCGATCCC 44

RESULT 5

AAH21229/C
 ID AAH21229 standard; DNA; 429 BP.

AC AAH21229;

DT 13-SEP-2001 (first entry)

DE *C. tropicalis* 16S rRNA DNA fragment YSASRSUG.

XX Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;

KW food monitoring; water monitoring; veterinary; forensic; primer; probe;

XX detection; ss.

OS *Candida tropicalis*.

PN WO200148237-A2.

PD 05-JUL-2001.

PF 27-DEC-2000; 2000WO-DE04610.

PR 23-DEC-1999; 99DE-1062895.

XX 31-MAY-2000; 2000DE-1027113.

PA (HOEF/) HOEF A.

XX (STUE/) STUEBER F.

PI Hoeft A, Stueber F;

DR WPI; 2001-425677/45.

XX

PT Rapid determination of microbial nucleic acid, useful e.g. for

PT diagnosing bacterial infections, by analysis of temperature-dependent

PT hybridization with oligonucleotides

XX

PS Disclosure: Figure 13; 57pp; German.

XX

CC This invention describes a novel method for detecting microbial DNA/RNA

CC (1) by concentrating (1) from a sample, adding at least one labeled

CC oligonucleotide (ON), performing temperature-dependent hybridization and

CC determining (1) from the physical properties of the (1)-ON complex, e.g.

CC the temperature dependence of hybridization. The method is used for rapid

CC determination of microbial genomic RNA or DNA, particularly for diagnosis

CC of bacterial infections (e.g. sepsis) or fungal infections (particularly

CC in intensive care patients), also for monitoring food and water, and for

CC veterinary or forensic investigations. The method provides quick

CC (typically less than 3 hours) quantitative and qualitative

CC determination/identification of microbial nucleic acid. It is very

CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231

CC represent primers and probes used to illustrate the method of the

XX invention.

SO Sequence 429 BP; 114 A; 85 C; 109 G; 119 T; 2 other;

Query Match 100.0%; Score 29; DB 22; Length 429;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAATAAGAACACACCGATCCC 29
 DB 408 GCGTCATTAATAAGAACACACCGATCCC 380

RESULT 6

AAH21230/C
 ID AAH21230 standard; DNA; 431 BP.


```

XX AC AAH21230;
XX DT 13-SEP-2001 (first entry)
XX DE C. albicans 16S rRNA DNA fragment YSASRSUA.
XX KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
XX KW food monitoring; water monitoring; veterinary; forensic; primer; probe;
XX KM detection; ss.
XX OS Candida albicans.
XX PN WO200148237-A2.
XX PD 05-JUL-2001.
XX PE 27-DEC-2000; 2000WO-DE04610.
XX PR 23-DEC-1999; 99DE-1062895.
XX PR 31-MAY-2000; 2000DE-1027113.
XX PA (HOEF/) HOEFT A.
XX PA (STUE/) STUEBER F.
XX PT Hoeft A, Stueber F;
XX PT WPI; 2001-425677/45.
XX DR
XX PT Rapid determination of microbial nucleic acid, useful e.g. for
XX PT diagnosing bacterial infections, by analysis of temperature-dependent
XX PT hybridization with oligonucleotides
XX PS Disclosure; Figure 13; 57pp; German.
XX XX
XX CC This invention describes a novel method for detecting microbial DNA/RNA
XX CC (I) by concentrating (I) from a sample, adding at least one labeled
XX CC oligonucleotide (ON), performing temperature-dependent hybridization and
XX CC determining (I) from the physical properties of the (I)-ON complex, e.g.
XX CC the temperature dependence of hybridization. The method is used for rapid
XX CC determination of microbial genomic RNA or DNA, particularly for diagnosis
XX CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
XX CC in intensive care patients), also for monitoring food and water, and for
XX CC veterinary or forensic investigations. The method provides quick
XX CC (typically less than 3 hours) quantitative and qualitative
XX CC determination/identification of microbial nucleic acid. It is very
XX CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
XX CC represent primers and probes used to illustrate the method of the
XX CC invention.
XX SQ Sequence 431 BP; 115 A; 86 C; 110 G; 120 T; 0 other;
XX
XX Query Match 100.0%; Score 29; DB 22; Length 431;
XX Best Local Similarity 100.0%; Pred. No. 0.037;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTCAATTAAGACACACACCGATCCC 29
DB 410 GCCTCAATTAAGACACACACCGATCCC 382
XX
XX RESULT 7
XX AAH21228/c
XX ID AAH21228 standard; DNA; 432 BP.
XX AC AAH21228;
XX DT 13-SEP-2001 (first entry)
XX DE C. parapsilosis 16S rRNA DNA fragment YSASRSUF.
XX KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
XX KW food monitoring; water monitoring; veterinary; forensic; primer; probe;

```

```

XX KM detection; ss.
XX XX
XX OS Candida parapsilosis.
XX XX
XX PN WO200148237-A2.
XX PD 05-JUL-2001.
XX PE 27-DEC-2000; 2000WO-DE04610.
XX PR 23-DEC-1999; 99DE-1062895.
XX PR 31-MAY-2000; 2000DE-1027113.
XX PA (HOEF/) HOEFT A.
XX PA (STUE/) STUEBER F.
XX PT Hoeft A, Stueber F;
XX PT WPI; 2001-425677/45.
XX DR
XX PT Rapid determination of microbial nucleic acid, useful e.g. for
XX PT diagnosing bacterial infections, by analysis of temperature-dependent
XX PT hybridization with oligonucleotides
XX PS Disclosure; Figure 13; 57pp; German.
XX XX
XX CC This invention describes a novel method for detecting microbial DNA/RNA
XX CC (I) by concentrating (I) from a sample, adding at least one labeled
XX CC oligonucleotide (ON), performing temperature-dependent hybridization and
XX CC determining (I) from the physical properties of the (I)-ON complex, e.g.
XX CC the temperature dependence of hybridization. The method is used for rapid
XX CC determination of microbial genomic RNA or DNA, particularly for diagnosis
XX CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
XX CC in intensive care patients), also for monitoring food and water, and for
XX CC veterinary or forensic investigations. The method provides quick
XX CC (typically less than 3 hours) quantitative and qualitative
XX CC determination/identification of microbial nucleic acid. It is very
XX CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
XX CC represent primers and probes used to illustrate the method of the
XX CC invention.
XX SQ Sequence 432 BP; 114 A; 86 C; 110 G; 121 T; 1 other;
XX
XX Query Match 100.0%; Score 29; DB 22; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 0.037;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTCAATTAAGACACACACCGATCCC 29
DB 411 GCCTCAATTAAGACACACACCGATCCC 383
XX
XX RESULT 8
XX AAT70913
XX ID AAT70913 standard; DNA; 28 BP.
XX AC AAT70913;
XX DT 12-MAR-2002 (first entry)
XX DE Probe CALA1038 for Candida species detection and quantitation.
XX XX
XX KM Candida albicans; Candida tropicalis; Candida dubliniensis;
XX KM Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX OS Candida albicans.
XX PN WO200183821-A2.
XX PD 08-NOV-2001.
XX PR 01-MAY-2001; 2001WO-US13884.
XX

```

PR 01-MAY-2000; 2000US-201249P.
 XX (GENP-) GEN-PROBE INC.
 XX Hogan JJ, Gordon PC;
 PI
 XX WPI; 2002-066537/09.
 DR
 XX Novel oligonucleotide sequences that are fully complementary to
 PT ribosomal RNA or DNA of *Candida* species, useful for detecting presence
 PT of *C. albicans*, *C. dubliniensis*, *C. viswanathii*, *C. parapsilosis* in test
 PT sample
 XX
 XX Claim 2; Page 26; 33pp; English.
 PS
 XX The present sequence is that of oligonucleotide probe CAL1038,
 CC which is complementary to a unique segment (see A170916) of the
 CC 18S ribosomal RNA of *Candida albicans*, *Candida tropicalis*, *Candida*
 CC *dubliniensis*, *Candida viswanathii* and *Candida troglitallis*. The
 CC probe is highly specific, and can distinguish these *Candida* species
 CC from their known phylogenetically nearest neighbours. It is
 CC useful for their detection and quantitation. Hybridisation to rRNA
 CC is enhanced by the presence of helper oligonucleotides, e.g. the Tm
 CC of hybridisation to *C. albicans* 18S rRNA increases from 57.8 to
 CC 63.2 degrees C in the presence of helper oligonucleotides CAL1005
 CC (see A170914) and CAL1066 (see A170912). The probe is an
 CC illustration of an oligonucleotide that: (1) hybridises the target
 CC nucleic acid under high stringency hybridisation conditions; (2)
 CC has a length of up to 100 nucleotide bases; and (3) includes at
 CC least 15 contiguous nucleotides falling within the sequence given
 CC in A170915 or its complement. It may include a detectable moiety,
 CC such as an acridinium ester or a radioisotope.
 XX
 SO Sequence 28 BP; 13 A; 8 C; 4 G; 3 T; 0 other;
 Query Match 96.6%; Score 28; DB 24; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCGTCATATTAAGAACACACACCGATCC 28
 DB 1 GCGTCATATTAAGAACACACACCGATCC 28
 RESULT 9
 AAF25849/C
 ID AAF25849 standard; DNA; 1776 BP.
 XX
 AC AAF25849;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE S. exiguus 18S rRNA encoding DNA.
 XX
 KW 18S rRNA; non-lactate-assimilating; Yeast; silage; aerobic stability;
 KW dry matter recovery; spoilage; animal feed; ds.
 KW
 OS Saccharomycetes exiguus.
 OS
 PN WO200104291-A1.
 PD
 XX 18-JAN-2001.
 PD
 XX 07-JUL-2000; 2000WO-US18744.
 XX
 PF 07-JUL-1999; 99US-0350710.
 PR
 XX (PION-) PIONEER HI-BRED INT INC.
 PA
 PI Hendrick CA, Platt NJ, Ruser BG, Hoganson DA;
 XX
 DR WPI; 2001-168421/17.
 XX

PT Non-lactate-assimilating yeast for improving the aerobic stability of
 PT silage, by inhibiting the growth of yeast strains associated with
 PT spoilage, using a strain of *Saccharomycetes exiguus* as inoculant
 XX
 XX Claim 27; Fig 3; 32pp; English.
 PS
 XX This invention describes a novel yeast strain useful as an inoculant for
 CC improving aerobic stability, by increasing dry matter recovery by
 CC reducing aerobic spoilage. The composition described in the method of the
 CC invention for use as a silage inoculant, comprises yeast strain SE24,
 CC SE136 or SE151, having ATCC accession numbers 74441, 74442 or 74443
 CC respectively, and optionally comprises their derivatives or mutants. The
 CC composition optionally comprises a carrier. The invention also describes
 CC a method for treating animal feed or silage susceptible to growth of
 CC spoilage organisms, by adding the yeast strain to feed, preferably upon
 CC ensiling and/or by maintaining the silage for 30 days or more. Also, a
 CC characteristic isolated DNA sequence which can be used to identify
 CC strains of *S. exiguus* which do not assimilate lactate and which inhibit
 CC growth of other yeast strains associated with the spoilage of silage.
 CC Also, an isolated yeast strain having a characteristic rRNA sequence or
 CC sequence that can be hybridized to it, which can also inhibit growth of
 CC yeast strains associated with aerobic spoilage, and which does not
 CC assimilate lactate. The process is useful for improving aerobic
 CC stability, by increasing dry matter recovery by reducing aerobic spoilage
 CC The inoculant is safe and nonhazardous as an additive
 XX
 SO Sequence 1776 BP; 474 A; 343 C; 453 G; 505 T; 1 other;
 Query Match 72.4%; Score 21; DB 22; Length 1776;
 Best Local Similarity 82.8%; Pred. No. 53;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 GCGTCATATTAAGAACACACACCGATCC 29
 DB 1067 GCGTCATATTAAGAACACACCGATCC 1039
 RESULT 10
 AAF23018/C
 ID AAF23018 standard; rRNA; 1802 BP.
 XX
 AC AAF23018;
 XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Yeast 18S rRNA sequence.
 XX
 KW Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
 KW *Mycobacterium*; *Enterococcus*; *Chlamydia*; *Mycoplasma*; *E. coli*; *Legionella*;
 KW *Salmonella*; *Pseudomonas*; *Campylobacter*; *Neisseria gonorrhoeae*; *Fungus*;
 KW *bacterium*, ss.
 XX
 OS Saccharomycetes cerevisiae.
 OS
 PN US6150517-A.
 PD
 XX 21-NOV-2000.
 PD
 XX 30-MAY-1995; 95US-0454063.
 PF
 XX 22-FEB-1994; 94US-0200866.
 PR
 XX 24-NOV-1987; 87US-0295208.
 PR
 XX 24-NOV-1987; 87WO-US03009.
 PR
 XX 11-DEC-1991; 91US-0806929.
 PR
 XX 24-NOV-1986; 86US-0934244.
 PR
 XX 07-AUG-1987; 87US-0083542.
 XX
 PA (GENP-) GEN-PROBE INC.
 PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
 XX
 DR WPI; 2001-060029/07.
 XX

PT Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to
PT hybridize to an rRNA region that distinguishes non-viral target from
PT non-viral non-target species.
XX
XX Disclosure: Fig 4; 75pp; English.
XX
XX The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
CC bacteria.
XX
SQ Sequence 1802 BP; 479 A; 351 C; 462 G; 510 U; 0 other:
Query Match 72.4%; Score 21; DB 22; Length 1802;
Best Local Similarity 82.8%; Pred. No. 53;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GCGTCATTAAAGAACACACCGATCCC 29
Db 1067 GGGTCATTAAAAAACACACCGATCCC 1039
RESULT 11
ABA99033
ID ABA99033 standard; DNA; 3420 BP.
XX
XX ABA99033;
XX
XX 20-MAY-2002 (first entry)
XX
DE Saccharomyces cerevisiae chromosome XII cosmid reading frame ORF YLR154C.
XX
XX Ecoc2.0; tree lineage; fibre length; wood density; fibre collapsibility;
KW fibre coarseness; growth rate; cell wall thickness; lignin content;
KW guaiacyl lignin content; syringyl lignin content; carbohydrate content;
KW kraft pulp yield; mechanical pulp energy demand; chemical pulping; fibre
KW quality; wood quality; YLR154C; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX
XX Key Location/Qualifiers
FH misc_feature 878..10537
FT /*tag= a
FT /note= "Ecoc2.0 probe complete sequence"
XX
XX WO200204663-A2.
XX
XX 17-JAN-2002.
XX
XX 21-JUN-2001; 2001WO-CA00927.
XX
XX 23-JUN-2000; 2000US-213585P.
XX
XX (PPCA) PULP & PAPER RES INST CANADA.
XX
XX Potter S, Watson PA;
XX
XX WPI: 2002-179711/23.
XX
XX
XX Identifying tree lineage for identifying trees having superior
PT phenotype, e.g. fibre length, comprises hybridizing a DNA probe to tree
PT genomic DNA isolated from spruce live tissue and assessing intensity of
PT the hybridization pattern
XX
XX
XX Disclosure: Fig 4; 48pp; English.
XX
XX The sequence represents a fragment of Saccharomyces cerevisiae chromosome
CC XII cosmid reading frame ORF YLR154C, including the complete sequence of
CC the Ecoc2.0 probe. The invention relates to a novel method for identifying
CC tree lineage capable of expressing desired biological and/or biochemical
CC phenotypes. The method is useful for identifying trees having superior

CC phenotype, including fibre length, wood density, fibre collapsibility,
CC fibre coarseness, cell wall thickness, growth rate, lignin content,
CC guaiacyl lignin content, syringyl lignin content, carbohydrate content,
CC kraft pulp yield, mechanical pulp energy demand, chemical uptake for
CC chemical pulping, extractive content and extractive compounds. The trees
CC include trees of the genus Pichia, Populus, Betula, Abies, Larix, Taxus,
CC Ulmus, Prunus, Quercus, Malus, Arbutus, Salix, Platanus, Acer, Tsuga,
CC Pseudotsuga, Pinus, Firaxinus, Eucalyptus, Acacia, Abrus, Cupressus,
CC Fagus, Juniperus, Thuja and Carya. The Ecoc2.0 probe is useful for
CC predicting wood or fibre quality.
XX
SQ Sequence 3420 BP; 1007 A; 853 C; 621 G; 939 T; 0 other:
Query Match 72.4%; Score 21; DB 24; Length 3420;
Best Local Similarity 82.8%; Pred. No. 55;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GCGTCATTAAAGAACACACCGATCCC 29
Db 1590 GGGTCATTAAAAAACACACCGATCCC 1618
RESULT 12
ABV50391
ID ABV50391 standard; cDNA; 568 BP.
XX
XX ABV50391;
XX
XX 17-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 50382.
XX
DE Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-218007P.
XX
XX 13-DEC-2000; 2000US-235281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 9808; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 SO Sequence 568 BP; 211 A; 109 C; 85 G; 162 T; 1 other;
 Query Match 69.7%; Score 20.2; DB 23; Length 568;
 Best Local Similarity 88.0%; Pred. No. 1e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCGTCATTAAGAACACACCGA 25
 DB 55 GCGTATTTAAAGAACACACCGA 79
 RESULT 13
 ID ABQ49302 standard; DNA; 1078 BP.
 AC ABQ49302;
 AT 12-JUL-2002 (first entry)
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35893.
 XX
 KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 OS Homo sapiens.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PE 01-SEP-2001; 2001WO-EP10074.
 PF 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 DR WPI: 2002-371829/40.
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in

CC the disclosure of the invention.
 XX
 SO Sequence 1078 BP; 154 A; 128 C; 385 G; 411 T; 0 other;
 Query Match 69.0%; Score 20; DB 24; Length 1078;
 Best Local Similarity 82.1%; Pred. No. 1.3e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 CGTCATTAAGAACACACCGATCCC 29
 DB 902 CGATTAAGAACACACCGATCCC 875
 RESULT 14
 ID ABQ49303 standard; DNA; 1078 BP.
 AC ABQ49303;
 AT 12-JUL-2002 (first entry)
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35894.
 XX
 KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 OS Homo sapiens.
 PN WO200218632-A2.
 PD 07-MAR-2002.
 PE 01-SEP-2001; 2001WO-EP10074.
 PF 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 DR WPI: 2002-371829/40.
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 SO Sequence 1078 BP; 411 A; 385 C; 128 G; 154 T; 0 other;

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:26:11 ; Search time 710.047 Seconds

(without alignments)
1670.846 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 29

Sequence: 1 gcgcataaagacacacacacgaccc 29

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
9: gb_dr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pin: *
35: em_hlg_rod: *
36: em_hlg_mam: *
37: em_hlg_vrt: *
38: em_sy: *
39: em_hlg_hum: *
40: em_hlg_mus: *
41: em_hlg_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	AX045494	AX045494 Sequence
2	29	100.0	29	AX298059	AX298059 Sequence
3	29	100.0	113	AX298065	AX298065 Sequence
4	29	100.0	113	AX298066	AX298066 Sequence
5	29	100.0	510	AF247474	AF247474 Unidentif
6	29	100.0	1029	AB030915	AB030915 Candida p
7	29	100.0	1632	AF114470	AF114470 Candida a
8	29	100.0	1670	AY227019	AY227019 Candida p
9	29	100.0	1700	CAJ5123	CAJ5123 Candida p
10	29	100.0	1723	VSASRSUH	VSASRSUH Candida a
11	29	100.0	1736	VSASRSUG	VSASRSUG Candida a
12	29	100.0	1739	VSASRSUF	VSASRSUF Candida l
13	29	100.0	1766	AB013533	AB013533 Candida s
14	29	100.0	1767	AB013549	AB013549 Candida s
15	29	100.0	1768	AB013589	AB013589 Candida v
16	29	100.0	1769	AB013586	AB013586 Candida a
17	29	100.0	1769	AB013588	AB013588 Candida a
18	29	100.0	1782	AY055856	AY055856 Candida p
19	29	100.0	1783	AY055855	AY055855 Candida p
20	29	100.0	1783	AY055857	AY055857 Candida p
21	29	100.0	1785	VSASRRNB	VSASRRNB Candida p
22	29	100.0	1787	VSASRSUA	VSASRSUA Candida tro
23	29	100.0	1788	AK069785	AK069785 Sequence
24	29	100.0	1788	E15168	E15168 Candida alb
25	29	100.0	1788	CAL165	X53497 Candida alb
26	29	100.0	1791	CD185SRNA	X99399 C.dublinien
27	28	96.6	28	AX298063	AX298063 Sequence
28	27.4	94.5	741	AF290987S2	AF290987 Candida t
29	27.4	94.5	1747	AB054292	AB054292 Candida sp
30	27.4	94.5	1753	LECBS18SR	X78600 L.elongispor
31	27.4	94.5	1772	AB013529	AB013529 Candida s
32	27.4	94.5	1773	AB013560	AB013560 Candida a
33	25.8	89.0	1020	AB030914	AB030914 Debaryomy
34	25.8	89.0	1038	AB030913	AB030913 Debaryomy
35	25.8	89.0	1043	CKU63036	AY249514 Candida xes
36	25.8	89.0	1363	AY249514	AY249514 Candida gu
37	25.8	89.0	1701	AY227020	AY227020 Candida gu
38	25.8	89.0	1717	AB105434	AB105434 Candida fa
39	25.8	89.0	1734	AB022440	AB022440 Debaryomy
40	25.8	89.0	1748	AB054280	AB054280 Candida gu
41	25.8	89.0	1750	AB054272	AB054272 Candida st
42	25.8	89.0	1750	AB070855	AB070855 Candida s
43	25.8	89.0	1750	AB106350	AB106350 Candida z
44	25.8	89.0	1751	AB054260	AB054260 Debaryomy
45	25.8	89.0	1751	AB054260	AB054260 Debaryomy

ALIGNMENTS

RESULT 1
AX045494
LOCUS AX045494 29 bp DNA
DEFINITION Sequence 55 from Patent WO0066789.
ACCESSION AX045494
VERSION AX045494.1 GI:11343957
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
Hogan, J.J.
AUTHORS
TITLE Polynucleotide matrix-based method of identifying microorganisms
JOURNAL Patent: WO 0066789-A 55 09-NOV-2000;
Gen-Probe Incorporated (US)

Pred. No. 15 is the number of results predicted by chance to have a

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FEATURES
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    Location/Qualifiers
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        /mol_type="genomic DNA"
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        /note="Probe for hybridizing ribosomal nucleic acids of a
        plurality of fungi in the genus Candida"
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ORIGIN
Query Match      100.0%; Score 29; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 1 GCCTCAATAAAGACACACACCGATCCC 29

RESULT 2
AX298059
LOCUS      AX298059      29 bp      DNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 1 from Patent WO0183821.
ACCESSION  AX298059
VERSION     AX298059.1 GI:17128145
KEYWORDS
SOURCE      Candida albicans
ORGANISM    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
  AUTHORS    Hogan, J.J. and Gordon, P.C.
  TITLE      Polynucleotide probes for detection and quantitation of Candida
  JOURNAL    Patent: WO 0183821-A 1 08-NOV-2001;
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 1 GCCTCAATAAAGACACACACCGATCCC 29

RESULT 3
AX298065
LOCUS      AX298065      113 bp      DNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 7 from Patent WO0183821.
ACCESSION  AX298065
VERSION     AX298065.1 GI:17128151
KEYWORDS
SOURCE      Candida albicans
ORGANISM    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
  AUTHORS    Hogan, J.J. and Gordon, P.C.
  TITLE      Polynucleotide probes for detection and quantitation of Candida
  JOURNAL    Patent: WO 0183821-A 7 08-NOV-2001;
  FEATURES
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      Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 42 GCCTCAATAAAGACACACACCGATCCC 70

RESULT 4
AX298066/c
LOCUS      AX298066      113 bp      mRNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 8 from Patent WO0183821.
ACCESSION  AX298066
VERSION     AX298066.1 GI:17128152
KEYWORDS
SOURCE      Candida albicans
ORGANISM    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
  AUTHORS    Hogan, J.J. and Gordon, P.C.
  TITLE      Polynucleotide probes for detection and quantitation of Candida
  JOURNAL    Patent: WO 0183821-A 8 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..113
          /organism="Candida albicans"
          /mol_type="mRNA"
          /db_xref="taxon:5476"
BASE COUNT      28 a          23 c          27 g          35 t
ORIGIN
Query Match      100.0%; Score 29; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 72 GCCTCAATAAAGACACACACCGATCCC 44

RESULT 5
AF247474/c
LOCUS      AF247474      510 bp      DNA      linear      PLN 06-FEB-2003
DEFINITION Unidentified saccharomycetalean sp. SPT1 18S ribosomal RNA, partial
            sequence.
ACCESSION  AF247474
VERSION     AF247474.1 GI:7716602
KEYWORDS
SOURCE      saccharomycete isolate SPT1
ORGANISM    saccharomycete isolate SPT1
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            unclassified Saccharomycetes.
REFERENCE
  AUTHORS    Trosok, S.P., Luong, J.H., Juck, D.F. and Driscoll, B.T.
  TITLE      Characterization of two novel yeast strains used in mediated
            biosensors for wastewater
  JOURNAL    Can. J. Microbiol. 48 (5), 418-426 (2002)
  MEDLINE    22104291
  PUBMED     12109881
  REFERENCES  2 (bases 1 to 510)
            Trosok, S.P., Driscoll, B.T. and Luong, J.H.

```

TITLE Direct Submission
JOURNAL Submitted (20-MAR-2000) Natural Resource Sciences, McGill University, 21,111 Lakeshore Rd., Ste-Anne-de-Bellevue, PQ H9X 3V9, Canada

FEATURES
Source
 1. 510
 /organism="Saccharomycete isolate SP1"
 /mol_type="genomic DNA"
 /isolate="SP1"
 /db_xref="taxon:123505"
 /country="Canada: Quebec, Thurso"
 /note="Isolated from pulp mill effluent"
 <1..>510
 /product="18S ribosomal RNA"

BASE COUNT
 139 a 87 c 126 g 158 t

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 29; DB 8; Length 510;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
 1 GCGTCATTAAGAAACAACCGATCCC 29
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 462 GCGTCATTAAGAAACAACCGATCCC 434

Db
 462 GCGTCATTAAGAAACAACCGATCCC 434

RESULT 6
LOCUS AB030915 1029 bp DNA linear PLN 19-AUG-1999
DEFINITION Candida parapsilosis gene for 18S rRNA, partial sequence.
ACCESSION AB030915
VERSION AB030915.1 GI:5738919
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Candida parapsilosis
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1029)
REFERENCE
AUTHORS Shintani, T. and Matsumoto, Y;
JOURNAL Candida parapsilosis gene for 18S rRNA, partial sequence
REFERENCE
AUTHORS Published Only in Database (1999)
TITLE 2 (bases 1 to 1029)
JOURNAL Shintani, T. and Matsumoto, Y.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process; 487-2 Kumekebota, Matsuyama, Ehime 791-1101 Japan
 (E-mail:shintani@rti.pref.ehime.jp, URL:www.rti.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES
Source
 1. 1029
 /organism="Candida parapsilosis"
 /mol_type="genomic DNA"
 /strain="IEY2"
 /db_xref="taxon:5480"
 <1..>1029
 /product="18S ribosomal RNA"

BASE COUNT
 291 a 195 c 249 g 294 t

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 29; DB 8; Length 1029;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
 1 GCGTCATTAAGAAACAACCGATCCC 29
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 1010 GCGTCATTAAGAAACAACCGATCCC 982

Db
 1010 GCGTCATTAAGAAACAACCGATCCC 982

RESULT 7
LOCUS AF114470 1632 bp DNA linear PLN 25-MAR-1999
DEFINITION Candida albicans 18S ribosomal RNA gene, complete sequence.

ACCESSION AF114470
VERSION AF114470.1 GI:4512045
KEYWORDS
SOURCE Candida albicans
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1632)
REFERENCE
AUTHORS Morris, M. L., Andrews, R. H., Rogers, A. H. and Ellis, D. H.
TITLE 18S rRNA gene full sequence for the type strain of Candida albicans, CBS 562
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 1632)
JOURNAL Morris, M. L., Andrews, R. H., Rogers, A. H. and Ellis, D. H.
DEFINITION Direct Submission
TITLE Submitted (16-DEC-1998) Dentistry, University of Adelaide, North Terrace, Adelaide, SA 5005, Australia
FEATURES
Source
 1. 1632
 /organism="Candida albicans"
 /mol_type="genomic DNA"
 /strain="CBS 562"
 /db_xref="taxon:5476"
 <1..>1632
 /product="18S ribosomal RNA"

BASE COUNT
 433 a 319 c 427 g 452 t

ORIGIN

Query Match
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 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
 1 GCGTCATTAAGAAACAACCGATCCC 29
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 948 GCGTCATTAAGAAACAACCGATCCC 920

Db
 948 GCGTCATTAAGAAACAACCGATCCC 920

RESULT 8
LOCUS AY227019 1670 bp DNA linear PLN 01-APR-2003
DEFINITION Candida parapsilosis strain CCO 3 18S ribosomal RNA gene, partial sequence.
ACCESSION AY227019
VERSION AY227019.1 GI:29423630
KEYWORDS
SOURCE Candida parapsilosis
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1670)
REFERENCE
AUTHORS Sujaya, I. N., Tamura, Y., Tanaka, T., Yamaki, T., Ikeda, T., Kikushima, N., Yata, H., Yokota, A., Asano, K. and Tomita, F.
TITLE Molecular monitoring of Zygosaccharomyces rouxii strain M2 in miso fermentation
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 1670)
JOURNAL Sujaya, I. N., Tamura, Y., Tanaka, T., Yamaki, T., Ikeda, T., Kikushima, N., Yata, H., Yokota, A., Asano, K. and Tomita, F.
DEFINITION Direct Submission
TITLE Submitted (29-JAN-2003) Molecular Bioscience, Grad. Sch. of Agric. Hokkaido University, North 9 West 9, Sapporo, Hokkaido 0608589, Japan
FEATURES
Source
 1. 1670
 /organism="Candida parapsilosis"
 /mol_type="genomic DNA"
 /strain="CCO 3"
 /db_xref="taxon:5480"
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 /product="18S ribosomal RNA"

BASE COUNT
 449 a 328 c 432 g 461 t

ORIGIN

Query Match 100.0%; Score 29; DB 8; Length 1670;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAGAACACACCGATCCC 29
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 Db 968 GCCTCATATAAGAACACACCGATCCC 940

RESULT 9
 CAAJ5123 1700 bp DNA linear PLN 02-FEB-1999
 LOCUS Candida albicans SSU rRNA gene.
 DEFINITION AJ005123
 VERSION AJ005123.1 GI:3046725
 KEYWORDS small subunit ribosomal RNA; SSU rRNA gene.
 SOURCE Candida albicans
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1
 AUTHORS Kermann,M.L., Schuppeler,M., Paul,K.D., Schoenian,G. and Smith,M.T.
 TITLE Red-pigmented Candida albicans in patients with cystic fibrosis
 JOURNAL J. Clin. Microbiol. 37 (1), 278 (1999)
 MEDLINE 99136628
 PUBMED 9988594

REFERENCE 2 (bases 1 to 1700)
 AUTHORS Schuppeler,M.
 TITLE Direct Submission
 SUBMITTED (08-APR-1998) Schuppeler M., Medizinische Mikrobiologie und Hygiene, Universitätsklinikum der TU-Dresden, Duererstrasse 24, D-01307 Dresden, GERMANY
 JOURNAL Location/Qualifiers
 FEATURES 1..1700
 source /organism="Candida albicans"
 /mol_type="genomic DNA"
 /db_xref="taxon:5476"
 gene 1..1700
 /gene="SSU rRNA"
 rRNA <1..>1700
 /gene="SSU rRNA"
 /product="small subunit ribosomal RNA"
 BASE COUNT 457 a 328 c 443 g 471 t 1 others

Query Match 100.0%; Score 29; DB 8; Length 1700;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAGAACACACCGATCCC 29
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 Db 985 GCCTCATATAAGAACACACCGATCCC 957

RESULT 10
 YSASRSUH/c 1723 bp rRNA linear PLN 12-FEB-2001
 LOCUS C.vismwanathii small subunit ribosomal RNA.
 DEFINITION M60309
 ACCESSION M60309.1 GI:176368
 VERSION M60309.1 GI:176368
 KEYWORDS Candida viswanathii
 SOURCE Candida viswanathii
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1723)
 AUTHORS Barns,S.M., Lane,D.J., Sogin,M.L., Bibeau,C. and Weisburg,W.G.
 TITLE Evolutionary relationships among pathogenic Candida species and relatives
 JOURNAL J. Bacteriol. 173 (7), 2250-2255 (1991)
 MEDLINE 91177814
 PUBMED 2007550

FEATURES Location/Qualifiers

source 1..1723
 /organism="Candida viswanathii"
 /mol_type="rRNA"
 /db_xref="taxon:5486"
 /tissue_11b="ATCC 22891"
 rRNA 1..1723
 /product="small subunit ribosomal RNA"
 BASE COUNT 431 a 313 c 404 g 458 t 117 others

Query Match 100.0%; Score 29; DB 8; Length 1723;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAGAACACACCGATCCC 29
 |||||||||||||||||||||||||||||
 Db 1052 GCCTCATATAAGAACACACCGATCCC 1024

RESULT 11
 YSASRSUG/c 1736 bp rRNA linear PLN 12-FEB-2001
 LOCUS C.tropicalis small subunit ribosomal RNA.
 DEFINITION M60308
 ACCESSION M60308.1 GI:176367
 VERSION M60308.1 GI:176367
 KEYWORDS Candida tropicalis
 SOURCE Candida tropicalis
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1736)
 AUTHORS Barns,S.M., Lane,D.J., Sogin,M.L., Bibeau,C. and Weisburg,W.G.
 TITLE Evolutionary relationships among pathogenic Candida species and relatives
 JOURNAL J. Bacteriol. 173 (7), 2250-2255 (1991)
 MEDLINE 91177814
 PUBMED 2007550

FEATURES Location/Qualifiers

source 1..1736
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 /mol_type="rRNA"
 /db_xref="taxon:5482"
 /tissue_11b="ATCC 750"
 rRNA 1..1736
 /product="small subunit ribosomal RNA"
 BASE COUNT 440 a 320 c 411 g 465 t 100 others

Query Match 100.0%; Score 29; DB 8; Length 1736;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATATAAGAACACACCGATCCC 29
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 Db 1051 GCCTCATATAAGAACACACCGATCCC 1023

RESULT 12
 YSASRSUF/c 1739 bp rRNA linear PLN 12-FEB-2001
 LOCUS C.parapsilosis small subunit ribosomal RNA.
 DEFINITION M60307
 ACCESSION M60307.1 GI:176366
 VERSION M60307.1 GI:176366
 KEYWORDS Candida parapsilosis
 SOURCE Candida parapsilosis
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1739)
 AUTHORS Barns,S.M., Lane,D.J., Sogin,M.L., Bibeau,C. and Weisburg,W.G.
 TITLE Evolutionary relationships among pathogenic Candida species and relatives
 JOURNAL J. Bacteriol. 173 (7), 2250-2255 (1991)

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MEDLINE      91177814
PUBMED      2007550
FEATURES
SOURCE
Location/Qualifiers
1. 1739
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/mol_type="rRNA"
/db_xref="taxon:5480"
/tissue_1lb="ATCC 22019"
1. 1739
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Query Match      100.0%; Score 29; DB 8; Length 1739;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACGATCCC 29
|||||
Db      1054 GCGTCATTAAGAAACAACGATCCC 1026

RESULT 13
AB013533/c      1766 bp      DNA      linear      PLN 11-DEC-1999
LOCUS      AB013533
DEFINITION      Candida lodderae 18S rRNA gene, strain JCM 1601, partial sequence.
ACCESSION      AB013533
VERSION      AB013533.1 GI:4586721
KEYWORDS
SOURCE
ORGANISM      Candida viswanathii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
AUTHORS      Sugita,T. and Nakase,T.
TITLE      Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
JOURNAL      Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
MEDLINE      99204096
PUBMED      10188281
REFERENCE
2 (bases 1 to 1766)
AUTHORS      Sugita,T.
TITLE      Direct Submission
SUBMITTED (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hiroseawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
SOURCE
Location/Qualifiers
1. 1766
/organism="Candida viswanathii"
/mol_type="genomic DNA"
/strain="JCM 1601"
/db_xref="taxon:5486"
<1. 1766
/product="18S ribosomal RNA"
BASE COUNT      480 a      338 c      454 g      494 t
ORIGIN
Query Match      100.0%; Score 29; DB 8; Length 1766;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACGATCCC 29
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Db      1032 GCGTCATTAAGAAACAACGATCCC 1004

RESULT 14
AB013549/c      1767 bp      DNA      linear      PLN 11-DEC-1999
LOCUS      AB013549
DEFINITION      Candida sojae 18S rRNA gene, strain JCM 1644, partial sequence.
ACCESSION      AB013549

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VERSION      AB013549.1 GI:4586737
KEYWORDS
SOURCE
ORGANISM      Candida sojae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
AUTHORS      Sugita,T. and Nakase,T.
TITLE      Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
JOURNAL      Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
MEDLINE      99204096
PUBMED      10188281
REFERENCE
2 (bases 1 to 1767)
AUTHORS      Sugita,T.
TITLE      Direct Submission
SUBMITTED (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hiroseawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
SOURCE
Location/Qualifiers
1. 1767
/organism="Candida sojae"
/mol_type="genomic DNA"
/strain="JCM 1644"
/db_xref="taxon:52253"
<1. 1767
/product="18S ribosomal RNA"
BASE COUNT      483 a      339 c      452 g      493 t
ORIGIN
Query Match      100.0%; Score 29; DB 8; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACGATCCC 29
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Db      1033 GCGTCATTAAGAAACAACGATCCC 1005

RESULT 15
AB013589/c      1768 bp      DNA      linear      PLN 11-DEC-1999
LOCUS      AB013589
DEFINITION      Candida viswanathii 18S rRNA gene, strain JCM 9567, partial
sequence.
ACCESSION      AB013589
VERSION      AB013589.1 GI:4586777
KEYWORDS
SOURCE
ORGANISM      Candida viswanathii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
AUTHORS      Sugita,T. and Nakase,T.
TITLE      Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
JOURNAL      Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
MEDLINE      99204096
PUBMED      10188281
REFERENCE
2 (bases 1 to 1768)
AUTHORS      Sugita,T.
TITLE      Direct Submission
SUBMITTED (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hiroseawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
SOURCE
Location/Qualifiers
1. 1768
/organism="Candida viswanathii"
/mol_type="genomic DNA"
/strain="JCM 9567"

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rRNA /db_xref="taxon:5486"
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BASE COUNT 480 a 340 c 454 g 494 t
ORIGIN

Query Match 100.0%; Score 29; DB 8; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCATTAAGACACACACCGATCCC 29
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Db 1034 GCGTCATTAAGACACACACCGATCCC 1006

Search completed: August 6, 2003, 23:29:00
Job time : 711.047 secs